

GenCore version 5.1.3  
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CM nucleic - protein search, using frame\_plus\_n2p model

Run on: January 6, 2003, 01:16:09; Search time 46.5 Seconds  
(without alignments)

2768.174 Million cell updates/sec

Title: US-09-882-735-1

Perfect score: 941

Sequence: 1 datagfgrgtgcccccaatg gctaccaccagattgagaar 483

Scoring table:

BLOSUM62  
Xgapop 10.0, Xgapext 0.5  
Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 1816940

Minimum DR seq length: 0

Maximum DR seq length: 2000000000

Post processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

MODEL=frame\_n2p\_model -DEV=xlh  
Q=/cgn2.1/ncspc/spool/gcgnaa2735/runat/cgn12003/073942\_15203/app\_query.fasta\_1.647  
DR-A Geneseq 101002 -OFTT-fastan -SUFFIX=rag -MINMATCH=0.1 -LOOPEL=0  
LCOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi  
-LIST=45 -DOALIGN=200 -THP SCORE=PTH -THP MAX=100 -THP MIN=0 -ALIGN=15  
MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER US09882735 -CNCN 1 0 -cgnat cgn12003/073942\_15203 -N-PU=6 -LCPU=3  
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Y-WAPOP=10 -YGAPEXT=0.5 -DELPE=6 -DELEXT=7

Database: A Geneseq 101002.\*

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- 2: /SID32/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.\*
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- 19: /SID32/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.\*
- 20: /SID32/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.\*
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- 22: /SID32/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.\*
- 23: /SID32/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID
1	941	100.0	161	13	AA277496
2	941	100.0	161	19	AAW59664
3	941	100.0	161	19	AAW52767
4	941	100.0	161	20	AAW89233
5	941	100.0	161	22	AAW37676
6	941	100.0	211	20	AAW89225
7	941	100.0	280	22	AAW66479
8	941	100.0	309	16	AAW70108
9	941	100.0	311	20	AAW89229
10	941	100.0	336	18	AAW33360
11	941	100.0	366	20	AAW89228
12	941	100.0	371	11	AAW07449
13	941	100.0	397	20	AAW89227
14	941	100.0	417	20	AAW89226
15	941	100.0	420	20	AAW89224
16	941	100.0	451	16	AAW70107
17	941	100.0	455	12	AAW10986
18	941	100.0	455	12	AAW11082
19	941	100.0	455	13	AAW20787
20	941	100.0	455	13	AAW24000
21	941	100.0	455	14	AAW42059
22	941	100.0	455	16	AAW75084
23	941	100.0	455	20	AAW10934
24	941	100.0	455	20	AAW36266
25	941	100.0	455	21	AAW37800
26	941	100.0	455	21	AAW26984
27	941	100.0	455	21	AAW23446
28	941	100.0	455	21	AAW01336
29	941	100.0	455	22	AAW86817
30	941	100.0	455	22	AAW37697
31	941	100.0	455	22	AAW36677
32	941	100.0	455	23	AAW81649
33	941	100.0	455	23	AAW75764
34	941	100.0	547	16	AAW70104
35	941	100.0	884	16	AAW70103
36	941	100.0	900	16	AAW70103
37	941	100.0	1245	16	AAW70106
38	941	100.0	1604	16	AAW70105
39	938	99.7	455	11	AAW07451
40	932	99.0	433	14	AAW51032
41	932	99.0	443	14	AAW51033
42	932	99.0	455	14	AAW42197
43	932	99.0	455	14	AAW51034
44	931	98.9	455	12	AAW12550
45	930	98.9	909	19	AAW64485

ALIGNMENTS

RESULT 1  
AAW27496  
ID AAW27496 standard; protein, 161 AA.  
XX  
AC AAW27496;  
XX

DT 09-MAR-1993 (first entry)

DE Native 30 kD TNF inhibitor.

XX Tumour necrosis factor; ethylene glycol; pharmacokinetic;  
KW adult respiratory distress syndrome; rheumatoid arthritis;  
KW septic shock; pulmonary fibrosis; spacer.  
XX

OS Homo sapiens.

XX

PN W00216221-A.

XX

PD 01-OCT-1992.

XX 13-MAR-1992; 92WC-US92122.  
 PF 15-MAR-1991; 91US-0669862.  
 XX 17-JAN-1992; 92US-0344296.  
 PR (SYND ) SYNERGEN INC.  
 PA  
 XX  
 PI Arnes LG, Brewer MT, Evans RJ, Kohno T, Thompson RC;  
 XX  
 DE WPI, 1992-34893/42.  
 XX  
 XX New ethylene glycolated polypeptide(s) with improved  
 PT pharmacokinetic properties for treating e.g. TNF and IL-1  
 PT mediated diseases, e.g. adult respiratory distress syndrome,  
 PT rheumatoid arthritis, septic shock etc.  
 XX  
 PS Claim 54; Fig 2; 100pp; English.  
 XX  
 CC The sequence shows a native 30 kD TNF inhibitor which may be  
 CC modified to contain at least one non-native cysteine residue, pref.  
 CC at positions 1, 14, 105, 111 and/or 165. The non-native cysteine is  
 CC joined to a non-peptidic polymer, pref. monomethoxy PEG via  
 CC thio-ether bonds. Two such TNF inhibitor moles. may be linked via  
 CC this non-peptidic spacer. The modified polypeptides show improved  
 CC pharmacokinetic properties, i.e. increased mol. wt. hence reduced  
 CC clearance rate following s.c. or systemic administration, increased  
 CC sol. of native TNF inhibitors, and reduced antigenicity. The  
 CC polypeptides may be used for treatment of TNF mediated diseases such  
 CC as adult respiratory distress syndrome, pulmonary fibrosis, rheumatoid  
 CC arthritis, inflammatory bowel disease and septic shock. The same  
 CC method may be applied to the interleukin-1 receptor antagonist  
 CC IL-1ra. See also AAR27495.  
 CC  
 XX  
 SQ Sequence 161 AA;  
 Alignment Scores:  
 Pred. No.: 3,89e-86 Length: 161  
 Score: 941.00 Matches: 161  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 13 Gaps: 0  
 US-09-882-735-1 (1-483) x AAR27496 (1-161)  
 QY 1 GATAGTGTGTGTCCTCCAGGAAATATATATCCCTCAAAATAATTCGATTGCTGTACC 60  
 DE 1 AspserValCysProGlnGlyLysTyrIleHisProGlnAsnSerIleCysCysThr 20  
 CY 41 AAGTGTCAAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 120  
 DB 21 LysCysHisLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 40  
 CY 121 TGTAGGAGAGTGTAG 180  
 DB 41 CysArgGluCysGluSerGlySerPheThrAlaSerGluAsnHisLeuAlaHisCysLeu 60  
 CY 181 AAGTGTCAAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 240  
 DB 61 SerCysSerLysCysArgLysGluMetGlyGlnValGlnIleSerSerCysThrValAsp 80  
 CY 241 CGGAGACAGCGT 300  
 DB 81 ArgAspThrValCysGlyCysArgLysAsnGlnIleArgHisTyrIlePheSerGluAsnLeu 100  
 CY 301 TTTCAATGCTTCAATGCTTCAATGCTTCAATGCTTCAATGCTTCAATGCTTCAATGCT 360  
 DB 101 PheGlnCysPheAsnGlnCysSerLeuGlnAsnGlnIleThrValHisLeuSerCysGlnGln 120  
 CY 361 AAAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 420  
 DB 121 LysHisHisThrValCysThrCysHisAlaGlyPhePheLeuArgGluAsnGlnCysVal 140

QY 421 TCGTAGTACTGTAGAGAAAGCTGAGATGACCAAGATTGCTACCCAGATTGAG 480  
 DE 141 SerCysSerHisCysLysLysSerLeuGlnCysThrIleLeuCysLeuProGlnIleGln 160  
 QY 481 AAT 483  
 DB 161 Asn 161  
 RESULT 2  
 AAW59664  
 ID AAW59664 standard; Protein; 161 AA.  
 XX  
 AC AAW59664;  
 XX  
 DT 28-SEP-1998 (first entry)  
 XX  
 DE Human soluble tumour necrosis factor receptor type I.  
 XX  
 KW Human; tumour necrosis factor; TNF; TNF receptor type I;  
 KW inflammatory disease; leukaemia; TNF binding protein;  
 KW anti-inflammatory drug; methotrexates.  
 OS Homo sapiens.  
 XX  
 PH WC9824463-A2.  
 XX  
 PD 11-JUN-1998.  
 XX  
 PF 08-DEC-1997; 97MO-US22733.  
 XX  
 PR 09-JUL-1997; 97US-0052023.  
 PR 06-DEC-1996; 96US-0032587.  
 PR 23-JAN-1997; 97US-0036355.  
 PR 07-FEB-1997; 97US-0039315.  
 XX  
 PA (AMGE-) AMGEN INC.  
 XX  
 PI Bendelet AM, Edwards CK, Sennello RM;  
 XX  
 DP WPI; 1998-333039/29.  
 DR N-PSDB; AAV41548.  
 XX  
 PT Treatment of acute or chronic inflammatory disease, e.g. leukaemia -  
 PT by administering tumour necrosis factor binding protein and at least  
 PT one additional anti-inflammatory drug, e.g. methotrexate  
 XX  
 PS Disclosure; Fig 1; 104pp; English.  
 XX  
 CC This is the amino acid sequence of the human tumour necrosis factor  
 CC receptor type I, used in the method of the invention involving the  
 CC treatment of acute or chronic inflammatory disease such as leukaemia  
 CC by administering tumour necrosis factor binding protein and at least  
 CC one additional anti-inflammatory drug, e.g. methotrexate.  
 XX  
 SQ Sequence 161 AA;  
 Alignment Scores:  
 Pred. No.: 3,89e-86 Length: 161  
 Score: 941.00 Matches: 161  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 19 Gaps: 0  
 US-09-882-735-1 (1-483) x AAW59664 (1-161)  
 QY 1 GATAGTGTGTGTCCTCCAGGAAATATATATCCCTCAAAATAATTCGATTGCTGTACC 60  
 DB 1 AspserValCysProGlnGlyLysTyrIleHisProGlnAsnSerIleCysCysThr 20  
 QY 61 AAGTGTCAAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 120

Db 21 LysCysHisLysGlyThrTyrLeuTyrAsnAspCysProGlyProGlyGlnAspThrAsp 40  
 QY 121 TCACAGGACTTTCATAGAGGCTTCTTCAACGCTTCAGAAAACACCTCAGACACTGCCTC 180  
 Db 41 (CysArgGluCysGluSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu 60  
 QY 181 AGTATATCTAAATATATGAAATGAGTATGAGTATGAGTATGAGTATGAGTATGAGTAT 240  
 Db 61 SerCysSerLysCysArgLysGluMetGlyGlnValGluIleSerSerCysThrValAsp 80  
 QY 241 CGGAGACACCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300  
 Db 81 ArgAspThrValCysGlyCysArgLysAsnGlnTyrArgHisIstYrTrpSerGluAsnLeu 100  
 QY 301 TTCACATGTTCAATTCGAGGCTTCTGCTCAATGGGACCTGACCTCTCTCTGCGCAGGAG 360  
 Db 101 PheGlnCysPheAsnCysSerLeuCysLeuAsnGlyThrValHisLeuSerCysGlnGlu 120  
 QY 361 AAACACACACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTC 420  
 Db 121 LysGlnAsnThrValCysThrCysHisAlaGlyPheLeuArgGluAsnGluCysVal 140  
 QY 421 TCCTGTAGTAACTGTAAAGAAAGCTGAGTGCAGGAGTTGCTGCTACCCGACATTGAG 480  
 Db 141 SerCysSerAsnCysLysLysSerLeuGluCysThrLysLeuCysLeuProGlnIleGlu 160  
 QY 481 AAT 483  
 Db 161 Asn 161  
 RESULT 3  
 AAW52267  
 ID AAW52267 standard; Protein; 161 AA.  
 XX AAW52267;  
 AC  
 DT 29-JUN-1998 (first entry)  
 XX  
 DE Soluble tumour necrosis factor receptor.  
 KW Soluble tumour necrosis factor receptor; TNFR: TNF-mediated disease;  
 KW tumour necrosis factor binding protein; autoimmune disease; arthritis;  
 KW adult respiratory distress syndrome; cachexia/anorexia; cancer; therapy;  
 KW chronic fatigue syndrome; graft rejection; Alzheimer's disease; TNBP.  
 XX  
 OS Homo sapiens.  
 PN W09H01555-A2  
 XX  
 PD 15-JAN-1998.  
 XX  
 PF 09-JUL-1997; 97WO-US12244  
 XX  
 PR 04-MAR-1997; 97US-0039792  
 PR 09-JUL-1996; 96US-0021443  
 PR 06-DEC-1996; 96US-0032534  
 PR 23-JAN-1997; 97US-0037737  
 PR 07-FEB-1997; 97US-0039314  
 XX  
 PA (AMGEN) AMGEN INC.  
 XX  
 PI Edwards CK, Fisher EF, Kieft GL;  
 XX  
 DR WPI; 1998-101052/09.  
 DR N PSDB; AAV19801.  
 XX  
 PT Truncated and soluble forms of tumour necrosis factor receptor -  
 PT useful for treating diseases involving factor, e.g. arthritis and  
 PT adult respiratory distress syndrome  
 XX  
 PS Claim 1; Fig 1; 205pp; English.  
 XX  
 CC This sequence is the human soluble tumour necrosis factor receptor

CC (STNFR). The protein was used to make the truncated STNFR proteins of the  
 CC invention. The truncated STNFR proteins and tumour necrosis factor  
 CC binding proteins (TNBP) are used to treat any TNF-mediated disease,  
 CC e.g. arthritis, adult respiratory distress syndrome, cachexia/anorexia,  
 CC cancer, chronic fatigue syndrome, graft rejection, Alzheimer's disease,  
 CC and other autoimmune diseases. Cells transformed with a vector containing  
 CC DNA encoding the protein may be used for production of recombinant STNFR,  
 CC which may also be used for measuring the amount of STNFR in samples and  
 CC to raise antibodies against STNFR. TNBP may also be used in preparation  
 CC of therapeutic compositions for treating the above diseases. The STNFR  
 CC proteins are well suited to large scale production (since they lack the  
 CC deamidation site in region 111-126, so are more stable in vivo); contain  
 CC fewer disulphide bonds and fewer epitopes, making them less antigenic  
 CC than full-length proteins.

SQ Sequence 161 AA;

#### Alignment Scores:

Pred. No.: 3,89e-86 Length: 161  
 Score: 941.00 Matches: 161  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 19 Gaps: 0

US-09-882-735-1 (1-483) x AAW52267 (1-161)

QY 1 GATAGTGTGTCTCCCAAGGAGAAATATATCAACCTCAAAATATTCGTTCTATC 40  
 Db 1 AspSerValCysProGlnGlyLysTyrIleHisProGlnAsnSerIleCysThr 20  
 QY 61 AAGTGCACAAAGAACTATTTATTAATGACTGTCTAGAGGAGGAGGAGGAGGAGGAG 120  
 Db 21 LysCysHisLysGlyThrTyrLeuTyrAsnAspCysProGlyProGlyGlnAspThrAsp 40  
 QY 121 TGCAGGAGTGTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 160  
 Db 41 CysArgGluCysGluSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu 60  
 QY 181 AGTGTCTCCAAATGCGGAAATGCGTTCAGTGTGAGTATCTCTCTTCTGACACATGAG 240  
 Db 61 SerCysSerLysCysArgLysGluMetGlyGlnValGluIleSerSerCysThrValAsp 80  
 QY 241 CGGAGACACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300  
 Db 81 ArgAspThrValCysGlyCysArgLysAsnGlnTyrArgHisIstYrTrpSerGluAsnLeu 100  
 QY 301 TTCAGTGTCTCAATTCGAGGCTTCTGCTCAATGGGACCTGACCTCTCTCTGCGCAGGAG 360  
 Db 101 PheGlnCysPheAsnCysSerLeuCysLeuAsnGlyThrValHisLeuSerCysGlnGlu 120  
 QY 361 AAACAGAACACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420  
 Db 121 LysGlnAsnThrValCysThrCysHisAlaGlyPheLeuArgGluAsnGluCysVal 140  
 QY 421 TCCTGTAGTAACTGTAAAGAAAGCTGAGTGCAGGAGTTGCTGCTACCCGACATTGAG 480  
 Db 141 SerCysSerAsnCysLysLysSerLeuGluCysThrLysLeuCysLeuProGlnIleGlu 160  
 QY 481 AAT 483  
 Db 161 Asn 161

#### RESULT 4

ID AAW89233 standard; Protein; 161 AA.

XX AAW89233;

XX 04-MAR-1999 (first entry)

XX Tumour necrosis inhibitor 30 kDa protein.

XX





Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 22 Gaps: 0

US 09 882-735-1 (1-483) x AAB37676 (1-161)

QY 1 GATAGCTGTGTCCCAAGAAATATATCCACCTCAAAATAATTCGATTGCTGACC 60  
 DB 1 AspSerValCysProGlnGlyLysTyrIleHisProGlnAsnAsnSerIleCysCysThr 20

QY 61 AACTGTCATCAAAAGCACTTGTACATGACTGTCCAGAGCCCGGGCGAGATACGGAC 120  
 DB 21 LysCysHisLysGlyThrTyrLeuTyrAsnAspCysProGlyProGlyGlnAspThrAsp 40

QY 121 TCGAGTACTGTGTATATATGCTCTTCAACCGCTTCAGAAAAACCACTCAGACACTGCCCTC 180  
 DB 41 CysArgGluCysGluSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu 60

QY 181 AGCTGTCTCAATGCGGAAGAAATGGTGTGAGTGTGAGATCTCTTCTGACAGTGGAC 240  
 DB 61 SerCysSerLysCysArgLysGluMetGlyGlnValGluIleSerSerCysThrValAsp 80

QY 241 CGGACACACCTGTGTGTGTGCGAGAGACAGTACCGGCATTATTGAGTGAACCTT 300  
 DB 81 ArgAspThrValCysGlyCysArgLysAsnGlnTyrArgHisTyrTrpSerGluAsnLeu 100

QY 301 TTCAGTGTCTCAATGCGGAAGAAATGGTGTGAGTGTGAGATCTCTTCTGACAGTGGAC 360  
 DB 101 PheGlnCysPheAsnCysSerLeuCysLeuAsnGlyThrValHisLeuSerCysGlnGlu 120

QY 361 AAACACAACTACCTGTGTGTGTGCGAGAGACAGTACCGGCATTATTGAGTGAACCTT 420  
 DB 121 LysGlnAsnThrValCysThrCysHisAlaGlyPhePheLeuArgGluAsnGluCysVal 140

QY 421 TCCTGTAGTAACTGTAAAGAAAGCTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 480  
 DB 141 SerCysSerAsnCysLysLysSerLeuGluCysThrLysLeuCysLeuProGlnIleGlu 160

QY 481 AAT 483  
 DB 161 Asn 161

RESULT 6  
 AAW89225  
 ID AAW89225 standard, Protein, 211 AA.  
 AC AAW89225;  
 XX 04-MAR-1999 (first entry)  
 DE Tumour necrosis factor bp/osteoprotegerin construct TNFbp 4.0.  
 XX Tumour necrosis factor receptor 1; TNFR.1; inhibitor, osteoprotegerin;  
 KW CPG; chimeric; fusion; dimerisation domain; autoimmune disease;  
 KW inflammation; apoptosis.  
 XX Homo sapiens.  
 OS Synthetic.  
 XX W09849305 A1.  
 XX 05-NOV-1998.  
 PD 29-APR-1998; 98WO-US08631.  
 XX 01-MAY-1997; 97US-0850189.  
 XX (AMGE-) AMGEN INC.  
 XX Boyle WJ, Wooden S;  
 XX WPI; 1999-014661/03.  
 DR

XX New chimeric osteoprotegerin polypeptides - contain the  
 PT osteoprotegerin dimerisation domain and a heterologous sequence,  
 PT useful to treat TNF and TNFR-mediated disorders

XX Example 1; Fig 4; 92pp; English.

XX The present invention describes a chimeric polypeptide (A1), comprising  
 CC an osteoprotegerin (OPG) dimerisation domain fused to a heterologous  
 CC amino acid sequence. Also described are: (1) a multimer polypeptide  
 CC comprising covalently associated A1 monomers; (2) an isolated nucleic  
 CC acid encoding A1; (3) an expression vector comprising the nucleic acid  
 CC sequence; and (4) a host cell transformed or transfected with the  
 CC expression vector so that the nucleic acid is expressible. The products  
 CC from the present invention are useful to treat a variety of disorders  
 CC including those related to receptor binding. Compositions comprising  
 CC tumour necrosis factor (TNF)/OPG and TNF receptor (TNFR)/OPG chimeras  
 CC are used to treat TNF and TNFR-mediated disorders such as inflammation,  
 CC autoimmune diseases and disorders related to excessive apoptosis. The  
 CC chimeras are also useful for detecting molecules which interact with  
 CC fused heterologous sequences to identify potential new receptors and  
 CC ligands. The present sequence represents a TNFbp/OPG construct from  
 CC the example of the present invention for creating TNFbp/OPG fusion  
 CC proteins.

XX SQ Sequence 211 AA;

Alignment Scores:  
 Pred No: 4 2e-86 Length: 211  
 Score: 941.00 Matches: 161  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 20 Gaps: 0

US-09 882 735-1 (1-483) x AAW89225 (1 211)

QY 1 GATAGTGTGTGTCCCAAGAAATATATCCACCTCAAAATAATTCGATTGCTGACC 60  
 DB 41 AspSerValCysProGlnGlyLysTyrIleHisProGlnAsnAsnSerIleCysCysThr 60

QY 61 AAGTGGCACAAGCAACCTACTTAT 120  
 DB 61 LysCysHisLysGlyThrTyrLeuTyrAsnAspCysProGlyProGlyGlnAspThrAsp 80

QY 121 TGCAGGGAGTGTGAGAGCGCTCTTCAACCTTCAAAACCACTCACTCACTCACTCACTCACTCACT 180  
 DB 81 CysArgGluCysGluSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu 100

QY 181 AGCTGTCTCAATGCGGAAGAAATGGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 240  
 DB 101 SerCysSerLysCysArgLysGluMetGlyGlnValGluIleSerSerCysThrValAsp 120

QY 241 CGGACACACCTGTGTGTGTGCGAGAGACAGTACCGGCATTATTGAGTGAACCTT 300  
 DB 121 ArgAspThrValCysThrCysHisAlaGlyPhePheLeuArgGluAsnGluCysVal 140

QY 301 TTCAGTGTCTCAATGCGGAAGAAATGGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 360  
 DB 141 PheGlnCysPheAsnCysSerLeuCysLeuAsnGlyThrValHisLeuSerCysGlnGlu 160

QY 361 AAACACAACTACCTGTGTGTGTGCGAGAGACAGTACCGGCATTATTGAGTGAACCTT 420  
 DB 161 LysGlnAsnThrValCysThrCysHisAlaGlyPhePheLeuArgGluAsnGluCysVal 180

QY 421 TCCTGTAGTAACTGTAAAGAAAGCTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 480  
 DB 181 SerCysSerAsnCysLysLysSerLeuGluCysThrLysLeuCysLeuProGlnIleGlu 200

QY 481 AAT 483  
 DB 201 Asn 201



XX New hybrid peptide(s) for binding cytokine(s) - comprising a  
PT malaria parasite peptide capable of binding a red blood cell and  
PT a receptor peptide.  
XX  
XX  
XX  
XX Example A; Page 54-55; 93pp; English.  
XX  
XX Hybrid peptides for binding cytokines, comprising a malaria parasite  
CC (Plasmodium falciparum) peptide (capable of binding to a red blood  
CC cell (RBC)) and a receptor peptide are claimed. AAR70103-25 are examples  
CC of these hybrid peptides. AAR70108 is a fusion of tumour necrosis factor  
CC receptor (in accordance with H Loetscher et al Cell, Vol. 61, 351-359)  
CC and glycoprotein binding protein (GBP) homologue (GBP). The  
CC use of cytokine receptors not normally found on RBCs means that the  
CC cytokine can bind harmlessly to the RBC without deleterious effect.  
CC The RBC protects the hybrid peptides from excretion from the kidney, and  
CC due to steric hindrance prevents the cytokines binding to a receptor in  
CC another cell. GBP 130 or GBP4 are the pref. malaria parasite peptides  
CC used, others include EBA 175 (175 kDa erythrocyte binding antigen),  
CC PMMSA (pre major merozoite surface antigen) and the Duffy binding  
CC receptor molecule (eg. exhibited by plasmodium vivax). These peptides  
CC bind to pref. glycoprotein A, B and C, sialo glycoproteins, found on the  
CC surface of RBCs. The hybrid peptides are thus used to lower the levels of  
CC free cytokines in the circulation to reduce pathological damage.  
XX  
XX Sequence 309 AA;

## Alignment Scores:

Pred. No.: 4,66e-86 Length: 309  
Score: 941.00 Matches: 161  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 16 Gaps: 0

US-09-882-735-1 (1-483) x AAR70108 (1-309)

QY 1 GATAGTGTGTGTCCTCCCAAGAAATATATCCACCTTCAAAATAATTCGATTGCTGTACC 60  
Db 20 ASPSerValCysProGlnGlyLysTyrIleHisProGlnAsnAsnSerIleCysCysThr 39  
QY 61 AATGTGTCACAAAGAACTTACTTGTACATGACTGTCCAGGCCCGCGCAGGATACGGAC 120  
Db 40 LysCysHisLysGlyThrTyrLeuTyrAsnAspCysProGlyProGlyGlnAspThrAsp 59  
QY 121 TGCAGGAGGTGTGAGAGCCGCTCTTTCACCGCTTCAGAAACACCTCAGACACTGCCTC 180  
Db 60 CysArgGluCysGluSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu 79  
QY 181 AGTGTGCTCCAAATGCGGAAGAAATGGGTGAGGTGAGATCTCTTGTGACAGTGGAC 240  
Db 80 SerCysSerLysCysArgLysGluMetGlyGlnValGluIleSerSerCysThrValAsp 99  
QY 241 CTTGTCACACCGTGTGCTGTCAGGAAGAACAGTACCGGCATTATTGGAGTCAAAACCTT 300  
Db 100 ArgAspThrValCysGlyCysArgLysAsnGlnTyrArgHisTyrTrpSerGluAsnLeu 119  
QY 301 TTCAGTGTCTCAATTCGACGCTCTGCTCAATGGACCCGTGCACCTCTCTCTGCCAGGAG 360  
Db 120 PheGlnCysPheAsnCysSerLeuCysLeuAsnGlyThrValHisLeuSerCysGlnGlu 139  
QY 361 AAACACAAACCTGTGTCACCTGCGATGATGAGTTCTTCTTAAGAGAAAACGAGTGTCTC 420  
Db 140 LysGlnAsnThrValCysThrCysHisAlaGlyPheLeuArgGluAsnGluCysVal 159  
QY 421 TCTTCTAGTAACTGTGAAGAAAGCTGGAGTGCACGAAGCTTGTGCTACCCAGATTGAG 480  
Db 160 SerCysSerAsnCysLysLysSerLeuGluCysThrLysLeuCysLeuProGlnIleGlu 179  
QY 481 AAT 483  
Db 180 Asn 180

## RESULT 9

AAW89229  
ID AAW89229 Standard; Protein, 311 AA.  
XX  
AC AAW89229;  
XX  
XX 04-MAR-1999 (first entry)  
XX  
XX Tumour necrosis factor bp/osteoprotegerin construct TNFbp/104.  
XX  
XX Tumour necrosis factor receptor 1; TNFR-1; inhibitor; osteoprotegerin;  
KW OPG; chimeric; fusion; dimerisation domain; autoimmune disease;  
KW Inflammation; apoptosis.  
XX  
XX Homo sapiens.  
OS Synthetic.  
OS  
XX WO9849305-A1.  
XX  
XX 05-NOV-1998.  
PD  
XX 29-APR-1998; 98WO-US08631.  
PF  
XX 01-MAY-1997; 97US-0850188.  
PR  
XX (AMGE-) AMGEN INC.  
PA  
XX Boyle WJ, Wooden S;  
XX  
XX WPI; 1999-034661/03.  
DR  
XX  
XX New chimeric osteoprotegerin polypeptides - contain the  
PT osteoprotegerin dimerisation domain and a heterologous sequence,  
PT useful to treat TNF and TNFR-mediated disorders  
XX  
XX Example 1; Fig 4; 92pp; English.  
XX  
XX The present invention describes a chimeric polypeptide (A1), comprising  
CC an osteoprotegerin (OPG) dimerisation domain fused to a heterologous  
CC amino acid sequence. Also described are: (1) a multimer polypeptide  
CC comprising covalently associated A1 monomers; (2) an isolated nucleic  
CC acid encoding A1; (3) an expression vector comprising the nucleic acid  
CC sequence; and (4) a host cell transformed or transfected with the  
CC expression vector so that the nucleic acid is expressible. The products  
CC from the present invention are useful to treat a variety of disorders  
CC including those related to receptor binding. Compositions comprising  
CC tumour necrosis factor (TNF)/OPG and TNF receptor (TNFR)/OPG chimeras  
CC are used to treat TNF and TNFR-mediated disorders such as inflammation,  
CC autoimmune diseases and disorders related to excessive apoptosis. The  
CC chimeras are also useful for detecting molecules which interact with  
CC fused heterologous sequences to identify potential new receptors and  
CC ligands. The present sequence represents a TNFbp/OPG construct from  
CC the example of the present invention for creating TNFbp/OPG fusion  
CC proteins.  
XX  
XX Sequence 311 AA;

## Alignment Scores:

Pred. No.: 4,67e-86 Length: 311  
Score: 941.00 Matches: 161  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 20 Gaps: 0

US-09-882-735-1 (1-483) x AAW89229 (1-311)

QY 1 GATAGTGTGTGTCCTCCCAAGAAATATATCCACCTTCAAAATAATTCGATTGCTGTACC 60  
Db 41 ASPSerValCysProGlnGlyLysTyrIleHisProGlnAsnAsnSerIleCysCysThr 60  
QY 61 AAGTGCACAAAGGACCTACTGTGACAACTGCTCCAGGAGCCGCGCAGGATACGAC 120  
Db 180 Asn 180



XX 29-APR 1998; 98WU-US08631.  
 XX  
 XX 01-MAY-1997; 97US-0850188.  
 XX  
 XX (AMGE-) AMGEN INC.  
 XX  
 XX Hoyle WJ, Wooden S;  
 XX  
 XX WPI: 1999-034661/03.  
 XX  
 XX New chimeric osteoprotegerin polypeptides - contain the  
 XX osteoprotegerin dimerisation domain and a heterologous sequence,  
 XX useful to treat TNF and TNFR-mediated disorders  
 XX  
 XX Example 1; Fig 4; 92pp; English.

The present invention describes a chimeric polypeptide (A1), comprising an osteoprotegerin (OPG) dimerisation domain fused to a heterologous amino acid sequence. Also described are: (1) a multimer polypeptide comprising covalently associated A1 monomers; (2) an isolated nucleic acid encoding A1; (3) an expression vector comprising the nucleic acid sequence; and (4) a host cell transformed or transfected with the expression vector so that the nucleic acid is expressible. The products from the present invention are useful to treat a variety of disorders including those related to receptor binding. Compositions comprising tumour necrosis factor (TNF)/OPG and TNF receptor (TNFR)/OPG chimeras are used to treat TNF and TNFR-mediated disorders such as inflammation, autoimmune diseases and disorders related to excessive apoptosis. The chimeras are also useful for detecting molecules which interact with fused heterologous sequences to identify potential new receptors and ligands. The present sequence represents a TNFbp/OPG construct from the example of the present invention for creating TNFbp/OPG fusion proteins.

XX Sequence 366 AA;

Alignment Scores:  
 Pred. No.: 4,88e-86 Length: 366  
 Score: 941.00 Matches: 161  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 20 Gaps: 0

US 09 882-735-1 (1-483) x AAW89228 (1-366)

QY	1	GATACCTGTTCCTCCAAAGAAAATAATATCAACCTCAAAAAATAATTGGATTGTGTACC	60
Db	41	AspSerValCysProGlnGlyLysTyrIleHisProGlnAsnAsnSerIleCysCysThr	60
QY	61	AAGTGCCACAAGAAGACTTAATTGTACAACTGCTGCAGGCCCGGGCAGGATACGGAC	120
Db	61	LysCysHisLysGlyThrTyrLeuTyrAsnAspCysProGlyProGlyGlnAspThrAsp	80
QY	121	TGCAGGGAATGTGCAGCGGCTCCCTTCACCGTTTCAGAAACACCTCACACACTGCCTC	180
Db	81	CysArgGluCysGlnSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu	100
QY	181	AGCTGCTCCAAATGCGCAAAGAAATGGGTCAGGTGGAGATCTCTTCTTCAGACGTGGAC	240
Db	101	SerCysSerLysCysArgLysGluMetGlyGlnValGluIleSerSerCysThrValAsp	120
QY	241	CGGATACATCATCTTCTGATGATGAGAACAACTAGTACCGGCAATTATTGGAGTAAACCTT	300
Db	121	ArgAspThrValCysGlyCysArgLysAsnGlnTyrArgHisTyrTrpSerGluAsnLeu	140
QY	301	TTTATATCTTCTTAATTAAGCTCTGCTCAATGGAGCCGTCACCTCTCTCTGCAGGAG	360
Db	141	PheGlnTyrPheAsnCysSerLeuCysLeuAsnGlyThrValHisLeuSerCysGln3Iu	160
QY	361	AAACAAAAATATATCTTCTGATGAGTATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT	420

Db 161 LysGlnAsnThrValCysThrCysHisAlaGlyPheTheLeuArgGluAsnGluCysVal 180

QY 421 TCCTGTAGTAGTAACCTGTAAGAAAAATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 480

Db 181 SerCysSerAsnCysLysSerLeuGluCysThrLysLeuCysLeuProGlnIleGln 200

QY 481 AAT 483

Db 201 Asn 201

RESULT 12

AAR07449

ID AAR07449 standard; protein; 371 AA.

XX AAR07449;

DT 29-JAN-1991 (first entry)

DE Tumour Necrosis Factor-Binding Protein from pTNF-RP15 cDNA.

KW Tumour necrosis factor binding protein; TNF-RP, TNF-receptor;

KW pTNF-RP15; infectious disease; parasitic disease; cachexia;

KW autoimmune disease; shock.

OS Homo sapiens.

PN EP393438-A.

PD 24-OCT-1990.

XX 06-APR-1990; 90EP-0106624.

FF 21-JUN-1989; 89PF-3926282

PR 21-APR-1989; 89DE-3913101.

XX (BOEH ) BOEHRINGER INGELHEIMINT.

XX Hauptmann R, Himmler A, Maurer-Fogy I, Stratowa C;

DR WPI: 1990-321987/43.

N-PSRP; AAQ06282.

PT DNA encoding TNF binding protein and TNF-receptor - used in

PT tumour treatment and to understand mechanism to TNF action

XX Disclosure; Fig 1(1-3); 51pp; German.

XX Clone pTNF-RP15 was used to construct pADTNF-RP, for transfection of

CC e.g. COS7 cells. The expressed proteins are useful

CC prophylactically and therapeutically to control disorders which

CC involve the damaging effects of TNF alpha or beta (e.g. infections or

CC parasitic diseases, shock, cachexia, autoimmune diseases, adult

CC respiratory distress syndrome etc., or side effects of treatment with

CC TNF-alpha). They can also be used as diagnostic reagents for

CC assaying TNF and in study of TNF-receptor interactions.

XX See also AAQ06282-Q06285.

XX Sequence 371 AA;

Alignment Scores:

Pred. No.:	4,9e-86	Length:	371
Score:	941.00	Matches:	161
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	11	Gaps:	0

US-09-882-735-1 (1-483) x AAR07449 (1-371)

QY 1 GATAGTGTCTGTCTCCCAAGSAAATATATATCACTCAAAATATTCATTCATTCATTC 60

Db 41 AspSerValCysProGlnGlyLysTyrIleHisProGlnAsnSerIleCysCysThr 60

[illegible]

	acid encoding A1, (3) an expression vector comprising the nucleic acid sequence; and (4) a host cell transformed or transfected with the CC expression vector so that the nucleic acid is expressible. The product from the present invention are useful to treat a variety of disorders including those related to receptor binding. Compositions comprising CC tumour necrosis factor (TNF)/OPG and TNF receptor (TNFR)/OPG chimeras are used to treat TNF and TNFR-mediated disorders such as inflammatory autoimmune diseases and disorders related to excessive apoptosis. The CC chimeras are also useful for detecting molecules which interact with fused heterologous sequences to identify potential new receptors and ligands. The present sequence represents a TNFRp/OPG construct from CC the example of the present invention for creating TNFRp/OPG fusion proteins.
XX	Sequence    397 AA,
SQ	
Alignment Scores:	
Pred. No.:	4.99e-86
Score:	941.00
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	100.00%
DB:	20
	Gaps: 0
US-09-86; 735-1 (1-483) x AAM89227 (1-397)	
QY	1 GATACCTGTGTGTGGTCAAGAAATATATTAACCTTCGAATATGATTGGTGTTACC 60
Dd	41 AapserValcysProGInglnglySTyrlleHisProGlnAsnAsnSerIleCysCysThr 60
QY	61 AAGTCCGCATAAAGAAAGAACCTATTGTATATGATATGCAAGTCCGCGAGATAGAGAC 120
Dd	61 LysCysHisLysgLythrTYrLeuTyAsnAspCysProGlyProGlylAsnSphTrasp 80
QY	121 TGCAGGAGATGTACAGCGCGGTGCTTACCGGTTCACGAAAACCATCGATCGACTGCTC 180
Dd	81 CysArgGluCysGlnSerGlySerPheThrAlaSerGlnHisIleuArgHisCysIeu 100
QY	181 AGTTCTTCGAATATGCAAGAAAGAAATATGCTGAGTGAAGATTCTTCTTGCAAGTAGAC 240
Dd	101 SerCysSerLysCysAspLysGluMetGlyGlnValGlnIleSerSerCysThrValAsp 120
QY	241 CGGAGACCTGATGTGTGGGTGACAGAAACAACCTACCGGATATTGGAGTGAAGAACCCT 300
Dd	121 ArgAspThrValCysGlyCysHisLysAsnGlnITyrAlaHisIstyrTrpSerGluSnu 140
QY	301 TTCAGTGTTCGAATATGCAAGTATGCTGCTTCGAATATGCAAGCGTGAACCTCTCTCTG 360
Dd	141 PheGlnCysPheAsnCysSerLeuCysLeuAsnGlyThrValHisPheSerCysGlnGln 160
QY	361 AACATCAACACCGGTGACCTGTCATGCGAGTCTTCTTCTTCAAGAAAGACAGGTGTC 420
Dd	161 LysGlnAsnThrValCysThrCysHisAlaGlyPhePheIleuArgGluAsnGluCysVal 180
QY	421 TCCTTACTAATCTATAGAAAGCTGCGAGATGACCAAGATTGTGCTTACCCAGATTGAG 480
Dd	181 SerCysSerAsnCysLysLysSerIleuGluCysThrIlyLeuCysIleuProGlnIleGlu 200
QY	481 AAT 483
Dd	201 Asn 201
RESULT 14	
AAM89226	
ID	AAM89226 standard; Protein; 417 AA.
XX	
AC	AAM89226;
XX	
DT	04-MAR-1999 (first entry)
XX	
DE	Tumour necrosis factor bp/osteoprotegerin construct TNFRp/196.
XX	
NM	Tumou necrosis factor receptor 1; TNFR-1; inhibitor; osteoprotegerin;

ORF; chimeric; fusion; dimerisation domain; autoimmune disease; inflammation; apoptosis.

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# Worms and Bacteria

## CHAPTER 1

synthetic.

WC9849305-A1

CS-NOV-1998.

20-APR-1998. 99WC-

22-448-1778, 980-0308031.

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CI-MAY-1997; 9705-0850188.

(AMGE ) AMGEN INC.

Boyle WJ, Wooden S;  
WPT; 1999 014661/03.

New chimeric osteoprotegerin polypeptides - contain the osteoprotegerin dimerisation domain and a heterologous sequence, useful to treat TNF and TNFR-mediated disorders

Example 1; Fig 4; 92pp; English.

The present invention describes a chimeric polypeptide (A1), comprising an osteoprotegerin (OPG) dimerisation domain fused to a heterologous amino acid sequence. Also described are: (1) a multimer polypeptide comprising covalently associated A1 monomers; (2) an isolated nucleic acid encoding A1; (3) an expression vector comprising the nucleic acid sequence; and (4) a host cell transformed or transfected with the expression vector so that the nucleic acid is expressible. The products from the present invention are useful to treat a variety of disorders including those related to receptor binding. Compositions comprising tumour necrosis factor (TNF)/OPG and TNF receptor (TNFR)/OPG chimeras are used to treat TNF and TNFR-mediated disorders such as inflammation, autoimmune diseases and disorders related to excessive apoptosis. The chimeras are also useful for detecting molecules which interact with fused heterologous sequences to identify potential new receptors and ligands. The present sequence represents a TNFRp/OPG construct from the example of the present invention for creating TNFRp/OPG fusion proteins.

Sequence 417 AA:

ment scores:

ON

3.062-00  
941 00

### Matches

Conservative. 0

Matches.

## Index:

Gaps:

22

0 882.735 1 (1 493) x AAW89336 (1.417)

[illegible]

1 GATAGTGTGTCTCCCAAGGAAAATATATCCACCCCTCAAATAATTCGATTTCCTGTACC 60

\_\_\_\_\_

41 AspSerValCysProGlnGlyLysTyrIleHisProGlnAsnAsnSerIleCysCysThr 60

61 AGTGCCACAAAGGAACTACTTGTAATAAGCTGTCCAGCCAGGATACGGAC 12

\_\_\_\_\_

[illegible]

61 GYRQYNNHLYRQYTNLTGTLGGLYASIASRQYRQGLYRQGLYGLIASRQINRASP 80





GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

CM nucleic protein search, using frame\_plus\_n2p model

Run on: January 6, 2003, 03:41:57 ; Search time 14.5 Seconds  
(without alignments)

1960.175 Million cell updates/sec

Title: us-09-882-735-1

Perfect score: 941

Sequence: 1 gatagtgtgtccccaagg.....gctacccagattgagaat 483

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Ygapop 10 0 Ygapext 0 5  
Fgapop 6.0 Fgapext 7.0  
Delop 6.0 Delext 7.0

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 525148

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Issued Patents AA:  
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5: /cgm2\_6/ptodata/1/iaa/PTUS.COMB.pcp.\*  
6: /cgm2\_6/ptodata/1/iaa/backfiles1.pcp.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	941	100.0	280	3	US-08-974-022-46
3	941	100.0	280	4	US-08-795-445A-46
4	941	100.0	280	4	US-08-795-447A-46
5	941	100.0	280	4	US-08-974-186-46
6	941	100.0	280	4	US-08-795-446B-46
7	941	100.0	280	4	US-08-704-945D-132
8	941	100.0	336	4	US-08-804-166-8
9	941	100.0	336	4	US-08-910-991-8
10	941	100.0	455	1	US-08-050-319B-25
11	941	100.0	455	1	US-08-321-668-2
12	941	100.0	455	1	US-08-837-941-2

13	941	100.0	455	2	US-08-126-016-2
14	941	100.0	455	2	US-08-465-982-25
15	941	100.0	455	4	US-08-815-469-5
16	941	100.0	455	4	US-09-006-353A-3
17	941	100.0	455	4	US-09-527-236A-5
18	941	100.0	455	4	US-08-054-970-2
19	941	100.0	455	4	US-09-565-918-4
20	941	100.0	455	4	US-09-573-986-3
21	930.5	98.9	909	4	US-09-013-895A-4
22	930.5	98.9	909	4	US-09-448-868-4
23	928	98.6	285	4	US-08-804-166-6
24	928	98.6	285	4	US-08-910-991-2
25	925.5	98.4	453	4	US-09-086-483A-5
26	924	98.2	199	1	US-08-050-319B-48
27	924	98.2	199	2	US-08-465-982-48
28	921	97.9	197	4	US-08-828-683A-21
29	904	96.1	154	4	US-08-828-683A-12
30	900	95.6	153	4	US-08-219-237B-4
31	900	95.6	153	4	US-08-477-347-12
32	900	95.6	153	4	US-08-476-862-3
33	900	95.6	153	4	US-08-468-560C-4
34	873	92.8	154	2	US-08-232-087A-10
35	842.5	89.5	256	4	US-08-804-166-2
36	842.5	89.5	256	4	US-08-910-991-2
37	837	88.9	307	4	US-08-804-166-4
38	837	88.9	307	4	US-08-910-991-4
39	822	87.4	139	4	US-08-706-945C-129
40	746	79.3	167	1	US-08-050-319B-2
41	746	79.3	167	1	US-08-050-319B-57
42	746	79.3	167	2	US-08-465-982-2
43	746	79.3	167	2	US-08-465-982-57
44	731	77.7	124	1	US-08-050-319B-4
45	731	77.7	124	2	US-08-465-982-4

#### ALIGNMENTS

#### RESULT 1

US-09-326-394-2  
; Sequence 2, Application US/09326394  
; Patent No. 6306820  
GENERAL INFORMATION:  
; APPLICANT: Bendelle, Alison M.  
; APPLICANT: Sennello, Regina M.  
; APPLICANT: Edwards, Carl K.  
; TITLE OF INVENTION: COMBINATION THERAPY USING A TNF BINDING  
; TITLE OF INVENTION: PROTEIN FOR TREATING TNF-MEDIATED DISEASES  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Amgen Inc.  
; STREET: 1840 DeHavilland Drive  
; CITY: Thousand Oaks  
; STATE: CA  
; COUNTRY: US  
; ZIP: 91320-1789  
COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/326,394  
; FILING DATE: 08-DEC-1997  
CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/932,587  
; FILING DATE: 06-DEC-1996  
; PRIORITY APPLICATION DATA:  
; APPLICATION NUMBER: US 60/036,345  
; FILING DATE: 23-JAN-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/039,315  
; FILING DATE: 07-FEB-1997

PRIOR APPLICATION DATA:  
APPLICATION NUMBER:

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1 APPLICATION NUMBER: US 60/052,023
2 FILING DATE: 09-JUL-1997
3
4 ATTORNEY/AGENT INFORMATION:
5
6 NAME: ZINDICK, Thomas K.
7 REGISTRATION NUMBER: 32,185
8 REFERENCE/DOCKET NUMBER: A-430D
9 INFORMATION FOR SEQ ID NO. 2:
10
11 SEQUENCE CHARACTERISTICS:
12
13 LENGTH: 161 amino acids
14
15 TYPE: amino acid
16
17 TOPOLOGY: linear
18
19 MOLECULE TYPE: protein
20
21 US-09-326 394-2

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Alignment Scores:

Pred. No.:	2,936-87	Length:	161
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Percent Similarity:	100.00%	Conservative:	0
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Query Match:	100.00%	Indels:	0
DB:	4	Gaps:	0

US 09 882-735-1 (1-483) X US-09-326 394 2 (1-261)

QY	1	GAATAGAGTGGTGGCCCAAGAAAGAAATATCTCCACCTCAAAATATCTGATTCGGTACG	60
Dd	1	AspSerValCysProGlnGlyLysTyrIleHisProGlnAsnSerIleGlySerThr	20
QY	61	AAATGCTAAAGAGAACTACTTGTACAAATGACTGTCCAGGCGCCGGAGTAAAGATACGAC	120
Dd	21	LysCysHisLysGlyThrThrTyrLeuTyrAsnAspCysProIleProIleValAspThrAsp	40
QY	121	TGACAGAGATGATGAG	180
Dd	41	CysArgGlnCysGlnSerCysLeuPheThrIleSerGlnAsnHisLeuArgHisCysLeu	60
QY	181	AGTTGTTCAATTTGCGAAGAGAGAAATGAGTCAAGTCAATCTTTCTTGACACAGTGGAC	240
Dd	61	SerCysSerLysCysArgLysGlnMetGlyValValGlnIleSerSerCysThrValAsp	80
QY	241	CGAGAGACAGGCTGTGTGCTGTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	300
Dd	81	ArgAspThrValCysGlyCysArgLysAsnGlnTyrArgHisTyrTrpSerGlnAsnLeu	100
QY	301	TTTCAGATGTTTAAATTGAGAGCTTTGATTAATGAGAGAGAGAGAGAGAGAGAGAGAGAG	360
Dd	101	PheGlnCysPheAsnCysSerLeuCysLeuAsnGlyThrValHisLeuSerCysGlnGln	120
QY	361	AAACACAAACAAACGATGAGACAGCCGACATGAGAGAGTTCTCTCTTAAGAGAGAGAGGTC	420
Dd	121	LysGlnAsnThrValCysThrCysHisIleArgIlePhePheLeuArgGlnAsnGlnCysVal	140
QY	421	TGGGTAGTAACTTTTAAAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	480
Dd	141	SerCysSerAsnCysLysLysSerLeuGlnCysThrIleCysLysCysLeuProGlnIleGln	160
QY	481	AAT AAT 483	
Dd	161	Asn 161	

## RESULT 2

US-08-974-022-46  
Sequence 46, Application US/08974022  
Patent No. 6015558  
GENERAL INFORMATION  
APPLICANT: Boyle, William J.  
APPLICANT: Lacey, David L.  
APPLICANT: Calzone, Frank J.  
APPLICANT: Chapp, Ming-Shi  
TITLE OF INVENTION: OSTEOPTHOEPRININ  
NUMBER OF SEQUENCES: 53  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Amgen Inc.  
STREET: 1910 DeBovill

STREET: 1840 Dehavilland Drive  
CITY: Thousand Oaks  
STATE: California  
COUNTRY: USA  
ZIP: 91320-1789  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/974,022  
FILING DATE: 12-DEC-1995

PRIOR APPLIC

1 APPLICATION NUMBER: 08/577,788  
2  
3 FILING DATE:  
4  
5 ATTORNEY/AGENT INFORMATION:  
6  
7 NAME: Winter, Robert B.  
8 REFERENCE/DOCKET NUMBER: A-378  
9  
10 INFORMATION FOR SEQ ID NO: 46:  
11

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; LENGTH: 280 amino acids
;
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
US-08-974-022-46

Alignment Scores:
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Score: 941.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
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US-09-882-735-1 (1-483) x US-08-974-022-46 (1-280)
Length: 280
Matches: 161
Conservative: 0
Mismatch: 0
Indels: 0
Gaps: 0

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QY	1	GATAGTGTGTGTCCTCCCAAGAAATAATATTCACCTCAAAATAAATTCATTCTCTAC	60
Dd	41	AspSerValCysProIleGlnIyIysTrpYrIleHisProGlnIleHisnSerIleCysCysThr	60
QY	61	AAGTCCACAAAGAAAGAACTACTTGTATCAATGACTGTCCAGCCCGGGCCAGATACGAC	120
Dd	61	LysCysHisIysGlyThrTyrIleuTyrIleHisnAspCysProGlyProGlyGlnAspThrAsp	80
QY	121	TGCAGGAGGTGTAGAGCGGCTCTCTTACCGCTTCACAAAACCACTCCAGACATGCTCC	180
Dd	81	CysArgGluCysGlnSerGlySerPheThrIleSerGlnIleHisnIleuArgHisCysLeu	10
QY	181	AGCTGCTCCAATATGCCAAAGAAATGGGTGAGGTGAGATCTCTTCTTGCACATGAC	240
Dd	101	SerCysSerIlyCysArgIlySerGluMetGlyIleValIleIleSerSerCysThrValAsp	12
QY	241	CGGACACCGGTGTGTGGCTGCGACGAGAACGATCCGGATTAATGGAGTAAACCTT	300
Dd	121	ArgAspThrValCysGlyCysArgIlyAsnIleTyrIleArgIleCysTrpSerGlnAsnLeu	14
QY	301	TTCAGTGCCTTAATATTCGACGCTCTGCCTCATATGGACCGTGGACCTCTCTCCGAGAG	360
Dd	141	PheGlnCysPheHisnCysSerIleuIysIleuAsnGlyIleThrIleHisIleuSerCysGlnGlu	16
QY	361	AAACAGAACACCGTGTGCACTGCCATGCAAGTTCTTTTAAAGAAACGAGTGTGTC	420
Dd	161	LysGlnAsnThrValCysThrCysHisIleGlyPhePheIleuArgGlnAsnGluCysVal	18
QY	421	TCTGTATGTAACCTGTAAAGAAAACCTGGAGTGCACGAAGTTGTGCTACCCAGATTGAG	480
Dd	181	SerCysSerHisnCysIlyIysSerIleuGluCysThrIlyIysLeuIysIleuProGlnIleGlu	20
QY	481	AAT	483





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; APPLICATION NUMBER: 08/577,784
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/POCKET NUMBERS: A-178
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 280 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HIS 08 795,446B 46

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Alignment Scores:	3.38e-87	Length:	280
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6			
61	AAGTCCACAAAGCAACTACTTTGTACATGACTCTCCAGATCCCGGGGACATACGGAC	120	QY
7			
8			
61	LysCysHisLysGlyThrTyrLeuTyrAsnAspCysProGlyProGlyGlnAspThrAsp	80	Db
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121	TCACAGAGTTCAGACAGAGTCTTTTCACAGCTTAGAAAAACACCTCAGACACTGCTC	180	QY
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12			
81	CysArgThrLysGluSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu	100	Db
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181	ACTGCTCTCAAAATCTGAAATAGAGTCTCAATGTGAGATCTCTCTTCCACACAGTGTAC	240	QY
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16			
101	SerCysSerLysCysArgLysGluMetGlyGlnValGluIleSerSerCysThrValAsp	120	Db
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241	CGACACACGTGTGTGCTCTCAGAAAGAACAGTACCGGACATTATTGGATGAAAACTT	300	QY
19			
20			
121	ArgAspThrValCysGlyCysArgLysAsnGlnTyrArgHisTyrTrpSerGluAsnLeu	140	Db
21			
22			
301	TTCCAGTGTCTCAATTGCAGCCCTCCCTCAATGGACCGTGACCTCTCCTCCACAGAG	360	QY
23			
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161	AAACAGAACACCGTGTCTCATATGACAGTCTCTTTCTTAAGAGAAAAACGATGTGTC	420	QY
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161	LysGlnAsnThrValCysThrCysHisAlaGlyPhePheLeuArgGluAsnGluCysVal	180	Db
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421	TCCTCTACTACTTAAAGAAAGCCTGGAGTGCACGAAGTTGTGCCTACCCGAGATTGAG	480	QY
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481	AAT 483		QY
35			
36			
201	Asn 201		Db

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RESULT 7
US 08-7006-945D-132
US Sequence 132, Application US/08706945D
Patent No. 6369027
GENERAL INFORMATION:
APPLICANT: Boyle, William
APPLICANT: Lacey, David
APPLICANT: Calzone, Frank
APPLICANT: Chang, Ming-Shi
TITLE OF INVENTION: Osteoprotegerin
FILE REFERENCE: A-378CIP
CURRENT APPLICATION NUMBER: US/08/706
CURRENT FILING DATE: 1996-09-03

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; PRIOR APPLICATION NUMBER: 08/577,798
; PRIOR FILING DATE: 1995.12.22
; NUMBER OF SEQ ID NOS: 145
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 132
; LENGTH: 280
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-706-945D-132

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Pred. No.	3 386-87
Score:	941.00
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	100.00%
DB:	4
	Length:
	Matches:
	Conservative:
	Mismatches:
	Indels:
	Gaps:
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US-09 882 735 ; (1 483) x US-08 706 9455 132 (1 280)

[illegible]

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RESULT 8
US-08-804-166-8
; Sequence 8, Application US/08804166
; Patent No. 6193972
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; GENERAL INFORMATION:
;
; APPLICANT: Campbell, Robert K.
; APPLICANT: Jameson, Bradford A.
; APPLICANT: Chappel, Scott C.
; TITLE OF INVENTION: HYBRID PROT
;
; NUMBER OF SEQUENCES: 22
;
; CORRESPONDENCE ADDRESS:
;
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street N.E.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007

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QY 241 CAGACACCGTGTCTGTCAGTAAAGAAACAGTACCGGTCATTATTGGAGTGAAGAACTT 300  
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Db 143 LysGlnAsnThrValCysThrCysHisAlaGlyPhePheLeuArgGluAsnGluCysVal 162  
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QY 421 TCTGTATTAATTTAAAGAAAGCTGAGAGTGCAGAGTGTGTGCTCAACCCAGATTGAG 480  
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QY 481 AAT 483  
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Db 183 Asn 183  
RESULT 10  
US-08-050-319B-25  
; Sequence 25, Application US/08050319B  
; Patent No. 5633145  
; GENERAL INFORMATION:  
; APPLICANT: M. Feldmann, P.W. Gray,  
; APPLICANT: M.J.C. Turner, F.M. Brennan  
; TITLE OF INVENTION: Modified human TNFalpha (Tumor  
; TITLE OF INVENTION: Necrosis Factor alpha) Receptor  
; NUMBER OF SEQUENCES: 57  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Reed & Robbins  
; STREET: 635 Bryant Street  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94301  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, version #1.25  
; CURRENT APPLICATION NUMBER: US/08/050,319B  
; FILING DATE: 10 May 1993  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Robbins, Roberta L.  
; REGISTRATION NUMBER: 33,208  
; REFERENCE/DOCKET NUMBER: 5150-0030  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 617-8999  
; TELEFAX: (415) 327-3231  
; INFORMATION FOR SEQ ID NO: 25:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 455 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-050-319B-25  
Alignment Scores:  
Prod. No.: 3,83e-87 Length: 455  
Score: 941.00 Matches: 161  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 1 Gaps: 0  
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QY 121 TGCAGGAGTGTCTGAGAGCGGCTCCTTCACCGCTTCGAAAACGACCTCAGACATGTCTC 180  
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QY 181 AGCTGCTCCAAATGCGGAAAGAAATGAGTACGTTGAGTACGATATCTCTTTTTCACAGTTGAC 240  
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Db 101 SerCysSerLysCysArgLysGluMetGlyGlnValGlnIleSerSerCysThrValAsp 120  
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Db 121 ArgAspThrValCysGlyCysArgLysAsnGlnTyrArgHisIstYrTpsSerGluAsnLeu 140  
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QY 301 TTCCAGTGTCTTCAATTGACGCTCTGCTCAATGAGAGCTTCACTCTCTCTCTCTCTCTCT 360  
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Db 141 PheGlnCysPheAsnCysSerLeuCysLeuAsnGlyThrValHisLeuSerCysGlnGlu 160  
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QY 361 AAACAGAACACCGTGTGTCAGTAAAGAAACAGTACCGGTCATTATTGGAGTGAAGAACTT 420  
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Db 161 LysGlnAsnThrValCysThrCysHisAlaGlyPhePheLeuArgGluAsnGluCysVal 180  
|||||  
QY 421 TCTGTATTAATTTAAAGAAAGCTGAGAGTGCAGAGTGTGTGCTCAACCCAGATTGAG 480  
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Db 181 SerCysSerAsnCysLysLysSerLeuGluCysThrLysLeuCysLeuProGlnIleGlu 200  
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QY 481 AAT 483  
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Db 201 Asn 201  
RESULT 11  
US-08-321-668-2  
; Sequence 2, Application US/08321668  
; Patent No. 5665859  
; GENERAL INFORMATION:  
; APPLICANT: WALLACH, David  
; APPLICANT: BRAKEBUSCH, Cord  
; APPLICANT: VARELOMEEV, Eugene  
; APPLICANT: BATKIN, Michael  
; TITLE OF INVENTION: MOLECULES INFLUENCING THE SHEDDING OF  
; TITLE OF INVENTION: THE TNF RECEPTORS, THEIR PREPARATION AND THEIR USE  
; NUMBER OF SEQUENCES: 42  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK  
; STREET: 419 Seventh Street, N.W., Suite 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION NUMBER: US/08/321,668  
; FILING DATE: 12-OCT-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: IL 107268  
; FILING DATE: 12-OCT-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BROWDY, Roger L.  
; REGISTRATION NUMBER: 25,618  
; REFERENCE/DOCKET NUMBER: WALLACH=13  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-628-5197  
; TELEFAX: 202-737-3528





QY 481 AAT 483

Db 201 Asn 201

## RESULT 11

US-08-126-016-2

; Sequence 2, Application US/08126018

; Patent No. 5811261

; GENERAL INFORMATION:

; APPLICANT: WALLACH, DAVID

; APPLICANT: KOPHAR, YARON

; APPLICANT: KEMPER, OLIVER

; APPLICANT: ENGELMANN, HARTMUT

; APPLICANT: BEKERUSCH, COPD

; APPLICANT: ADERKA, DAN

; TITLE OF INVENTION: EXPRESSION OF THE RECOMBINANT TUMOR

; NUCLEOTIDE SEQUENCE: 26

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Browdy and Neimark

; STREET: 419 Seventh Street, N.W., Suite 300

; CITY: Washington

; STATE: DC

; COUNTRY: USA

; ZIP: 20004

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent in Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/126.016

; FILING DATE: 24-SEP-1993

; CLASSIFICATION: 435

; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER: US 07/625668

; FILING DATE: 13-DEC-1990

; ATTORNEY/AGENT INFORMATION:

; NAME: BROWDY, FOGEL L

; REGISTRATION NUMBER: 25,618

; REFERENCE/DOCKET NUMBER: WALLACH4

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202-628-5197

; TELEFAX: 202-747-4524

; TELEX: 248633

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 455 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US 08 126-016-2

## Alignment Scores:

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Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	2	Gaps:	0

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QY 61 AAGTCGCAAAAGCACTTGTACATGCTCCAGCGCGGCGGAGGATACCGAC 120

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Db 81 CysArgGluCysGluSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu 100

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QY 301 TTCAGTGTCTTCAATTCAGACCTCTGCTCTCAATGAGACCTGCTCTCTCTCTCTCT 600

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QY 361 AAACAGAACACCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420

Db 161 LysGlnAsnThrValCysThrCysHisAlaGlyPhePheLeuArgGluAsnGluCysVal 180

QY 421 TCCTGTAGTAACTGTAAGAAAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480

Db 181 SerCysSerAsnCysLysLysSerLeuGluCysThrLysLeuCysLeuProGlnIleGlu 200

QY 481 AAT 483

Db 201 Asn 201

## RESULT 14

US-08-465-982-25

; Sequence 25, Application US/08465982

; Patent No. 5863786

; GENERAL INFORMATION:

; APPLICANT: M.Feldmann, P.W. Gray,

; APPLICANT: M.J.C. Turner, F.M. Brennan

; TITLE OF INVENTION: Modified human TNFalpha (Tumor

; NUCLEOTIDE SEQUENCE: 57

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Peed &amp; Robbins

; STREET: 635 Bryant Street

; CITY: Palo Alto

; STATE: California

; COUNTRY: USA

; ZIP: 94301

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent in Release #1.0, version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/465,982

; FILING DATE:

; CLASSIFICATION:

; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER: US/08/050,319

; FILING DATE: 10-May-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Robbins, Roberta L.

; REGISTRATION NUMBER: 33,208

; REFERENCE/DOCKET NUMBER: 5150-0030

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 617-8999

; TELEFAX: (415) 327-3231

; INFORMATION FOR SEQ ID NO: 25:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 455 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-465-982-25

## Alignment Scores:

Pred. No.:	3-83e-87	Length:	455
Score:	941.00	Matches:	161



GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

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Run on: January 6, 2003, 03:44:00 / Search time 29.5 Seconds  
(without alignments)  
620.582 Million cell updates/sec

Title: US-09-882-735-1

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Searched: 117078 seqs, 18951520 residues

Total number of hits satisfying chosen parameters: 234156

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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2	941	100.0	161	9	US-09-882-735-4 Sequence 4, Appl
3	941	100.0	161	9	US-09-882-736-4 Sequence 4, Appl
4	941	100.0	161	10	US-09-882-737-4 Sequence 4, Appl

5	941	100.0	161	10	US-09-882-738-2 Sequence 2, Appl
6	941	100.0	162	9	US-09-882-739-6 Sequence 6, Appl
7	941	100.0	162	10	US-09-882-740-9 Sequence 9, Appl
8	941	100.0	162	10	US-09-882-741-22 Sequence 22, Appl
9	941	100.0	172	9	US-09-882-742-20 Sequence 20, Appl
10	941	100.0	173	9	US-09-882-743-16 Sequence 16, Appl
11	941	100.0	183	9	US-09-882-744-10 Sequence 10, Appl
12	941	100.0	190	9	US-09-882-745-19 Sequence 18, Appl
13	941	100.0	200	9	US-09-882-746-12 Sequence 12, Appl
14	941	100.0	221	9	US-09-882-747-14 Sequence 14, Appl
15	941	100.0	211	9	US-09-882-748-8 Sequence 8, Appl
16	941	100.0	213	9	US-10-125-062-1 Sequence 1, Appl
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18	941	100.0	371	9	US-09-792-356-12 Sequence 12, Appl
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21	941	100.0	455	9	US-09-882-751-17 Sequence 17, Appl
22	941	100.0	455	9	US-09-882-752-5 Sequence 5, Appl
23	941	100.0	455	9	US-09-882-753-2 Sequence 2, Appl
24	941	100.0	455	9	US-09-882-754-27 Sequence 27, Appl
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43	928	98.6	285	10	US-09-798-789-19 Sequence 19, Appl
44	927	98.5	162	10	US-10-112-793-21 Sequence 21, Appl
45	921	97.9	157	9	US-10-112-793-21 Sequence 21, Appl

#### ALIGNMENTS

RESULT 1  
US-09-882-734-4  
Sequence 4, Application US/09898234  
Patent No. US20020155112A1  
GENEPAL INFORMATION:  
APPLICANT: Hauptmann, Rudolph  
APPLICANT: Himmler, Adolf  
APPLICANT: Maurer-Fogy, Ingrid  
APPLICANT: Stralow, Christian  
TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for  
TITLE OF INVENTION: Them  
FILE REFERENCE: 98,385-1  
CURRENT APPLICATION NUMBER: US/99/898,234  
CURRENT FILING DATE: 2001-07-03  
PRIOR APPLICATION NUMBER: 09/525,998  
PRIOR FILING DATE: 2000-03-15  
PRIOR APPLICATION NUMBER: 08/383,676  
PRIOR FILING DATE: 1995-02-01  
PRIOR APPLICATION NUMBER: 08/153,287  
PRIOR FILING DATE: 1993-11-17  
PRIOR APPLICATION NUMBER: 07/821,750  
PRIOR FILING DATE: 1992-01-02  
PRIOR APPLICATION NUMBER: 07/511,430  
PRIOR FILING DATE: 1990-04-20  
NUMBER OF SEQ ID NOS: 87  
SOFTWARE: Patent In Ver. 2.0  
SEQ ID NO 4  
LENGTH: 161

TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-898-234-4

## Alignment Scores:

Pred. No.:	Score:	Percent Similarity:	Best Local Similarity:	Query Match:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
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US-09-882-735-1 (1-483) x US-09-898-234-4 (1-161)

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Db 21 LysCysHisLysGlyThrTyrIleuTyraAsnAspCysProGlyProGlyGlnAspThrAsp 40
CY 121 TGCAAGAGAGTGTGAGAGCGGCTCTCCACCGCTTCAGAAAACCACTCAGACACTGCCTC 180
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Db 41 CysArgGlnCysGlnSerGlySerPheThrAlaSerGlnAsnHisLysLeuArgHisCysLeu 60
CY 181 AGCTGTCCAAATGCGCAAAAGAAATGGGTCAAGTGGAGATCTCTTTCGACACTGGAC 240
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Db 61 SerCysSerLysCysArgLysGlnMetGlyGlnValGlnIleSerSerCysThrValAsp 80
CY 241 CGGAGACACCGTGTGTGCTGCTCAGAGAAACCACTCCGCAATTATTGAGTAAACCTT 300
    |||
Db 81 ArgAspThrValCysGlyCysArgLysAsnGlnTyrArgHisTyrTrpSerGlnAsnLeu 100
CY 301 TTCAGTGTCTCAATGTGACCTCTGCTCAATGGAGCGGTGACCTCTCCGCGCAGAG 360
    |||
Db 101 PheGlnCysPheAsnCysSerLeuCysLeuAsnGlyThrValHisLeuSerCysGlnGlu 120
CY 361 AAACAGAACACCGTGTGACCTCTGCTCAATGGAGCGGTGACCTCTCCGCGCAGAG 420
    |||
Db 121 LysGlnAsnThrValCysThrCysHisAlaGlyPhePheLeuArgGlnAsnGlnCysVal 140
CY 421 TCCGTGTACTACTGTAAAGAAACCGTGGAGTGCAGAAATGTCCTCCACGATTGAG 480
    |||
Db 141 SerCysSerAsnCysLysLysSerLeuGlnCysThrLysLeuCysLeuProGlnIleGlu 160
CY 481 AAT 483
    |||
Db 161 Asn 161

```

## RESULT 2

US-09-899-429A-4  
Sequence 4, Application US/09899429A  
Patent No. US20020169118A1  
GENERAL INFORMATION:  
APPLICANT: Hauptmann, Rudolph  
APPLICANT: Himmler, Adolph  
APPLICANT: Maurer-Fogy, Ingrid  
APPLICANT: Stratowa, Christian  
TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for  
FILE REFERENCE: 98-385-J  
CURRENT FILING DATE: 2001-07-03  
CURRENT APPLICATION NUMBER: US/09/899,429A  
PRIOR FILING DATE: 1995-02-23  
PRIOR APPLICATION NUMBER: 09/477,639  
PRIOR FILING DATE: 1995-06-07  
PRIOR APPLICATION NUMBER: 08/383,676  
PRIOR FILING DATE: 1995-02-01  
PRIOR APPLICATION NUMBER: 08/153,287  
PRIOR FILING DATE: 1993-11-17  
PRIOR APPLICATION NUMBER: 07/821,750

PRIOR FILING DATE: 1992-01-02  
PRIOR APPLICATION NUMBER: 07/511,430  
PRIOR FILING DATE: 1990-04-20  
NUMBER OF SEQ ID NOS: 97  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 4  
LENGTH: 161  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-899-429A-4

## Alignment Scores:

Pred. No.:	Score:	Percent Similarity:	Best Local Similarity:	Query Match:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
4.38e-80	941.00	100.00%	100.00%	100.00%	161	161	0	0	0	0

US-09-882-735-1 (1-483) x US-09-899-429A-4 (1-161)

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CY 1 GATAGTGTGTGTCCTCCCAAGAAATATATCCACCCCTCAAAATATTCGATTGCTGTACC 60
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Db 1 AspservAlCysProGlnGlyLysTyrIleHisProGlnAsnSerIleCysCysThr 20
CY 61 AAGTCCCAAAAGGAACTTACTGTACATGACTGTCCAGCCCGGAGGATACGAC 120
    |||
Db 21 LysCysHisLysGlyThrTyrIleuTyraAsnAspCysProGlyProGlyGlnAspThrAsp 40
CY 121 TGCAAGAGAGTGTGAGAGCGGCTCTCCACCGCTTCAGAAAACCACTCAGACACTGCCTC 180
    |||
Db 41 CysArgGlnCysGlnSerGlySerPheThrAlaSerGlnAsnHisLysLeuArgHisCysLeu 60
CY 181 AGCTGTCCAAATGCGCAAAAGAAATGGGTCAAGTGGAGATCTCTTTCGACACTGGAC 240
    |||
Db 61 SerCysSerLysCysArgLysGlnMetGlyGlnValGlnIleSerSerCysThrValAsp 80
CY 241 CGGAGACACCGTGTGTGCTGCTCAGAGAAACCACTCCGCAATTATTGAGTAAACCTT 300
    |||
Db 81 ArgAspThrValCysGlyCysArgLysAsnGlnTyrArgHisTyrTrpSerGlnAsnLeu 100
CY 301 TTCAGTGTCTCAATGTGACCTCTGCTCAATGGAGCGGTGACCTCTCCGCGCAGAG 360
    |||
Db 101 PheGlnCysPheAsnCysSerLeuCysLeuAsnGlyThrValHisLeuSerCysGlnGlu 120
CY 361 AAACAGAACACCGTGTGACCTCTGCTCAATGGAGCGGTGACCTCTCCGCGCAGAG 420
    |||
Db 121 LysGlnAsnThrValCysThrCysHisAlaGlyPhePheLeuArgGlnAsnGlnCysVal 140
CY 421 TCCGTGTACTACTGTAAAGAAACCGTGGAGTGCAGAAATGTCCTCCACGATTGAG 480
    |||
Db 141 SerCysSerAsnCysLysLysSerLeuGlnCysThrLysLeuCysLeuProGlnIleGlu 160
CY 481 AAT 483
    |||
Db 161 Asn 161

```

## RESULT 3

US-09-792-356-4  
Sequence 4, Application US/09792356  
Publication No. US20020183485A1  
GENERAL INFORMATION:  
APPLICANT: Hauptmann, Rudolph  
APPLICANT: Himmler, Adolph  
APPLICANT: Maurer-Fogy, Ingrid  
APPLICANT: Stratowa, Christian  
TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for  
FILE REFERENCE: 98-385-G  
CURRENT FILING DATE: 2001-08-17  
CURRENT APPLICATION NUMBER: US/09/792,356  
PRIOR FILING DATE: 1995-06-07

FILE REFERENCE: 98,385-H  
CURRENT APPLICATION NUMBER: US/09/899,422  
CURRENT FILING DATE: 2001-08-21  
PRIOR APPLICATION NUMBER: 09/525,998  
PRIOR FILING DATE: 2000-03-15  
PRIOR APPLICATION NUMBER: 08/383,676  
PRIOR FILING DATE: 1998-02-01  
PRIOR APPLICATION NUMBER: 08/153,287  
PRIOR FILING DATE: 1993-11-17  
PRIOR APPLICATION NUMBER: 07/821,750  
PRIOR FILING DATE: 1992-01-02  
PRIOR APPLICATION NUMBER: 07/511,430  
NUMBER OF SEQ ID NOS: 87  
SOFTWARE: Patent In Ver. 2.0  
SEQ ID NO 4  
LENGTH: 161  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-899-422-4

Alignment Scores:  
Pred. No.: 4,398-80 Length: 161  
Score: 941.00 Matches: 161  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 9 Gaps: 0

US-09-882-735-1 (1-483) x US-09-792-356-4 (1-161)

QY 1 GATAGTGTGTGTCCTCCCAAGGAAATATATACACCTCAAAATAATTCGATTGCTGTACC 60  
DB 1 AspSerValCysProGlnGlyLysTyrIleHisProGlnAsnSerIleCysCysThr 20  
QY 61 AAGTCCCAAGGAAACCTATTGTACAAATGACTGTCCAGCCCGGGCGGAGGATACGGAC 120  
DB 21 LysCysHisLysGlyThrTyrLeuTyrAsnAspCysProGlyProGlyGlnAspThrAsp 40  
QY 121 TGCAGGAGTGTGAGAGGCGCTCTTCCACCGCTTCAGAAAACACCTCAGACACTGCTC 180  
DB 41 CysArgGluCysGluSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu 60  
QY 181 AGCTGTCCAAATGCCAAAGAAATGGGTGAGTGGAGATCTCTTTCACAGTGGAC 240  
DB 61 SerCysSerLysCysArgLysGluMetGlyGlnValGluIleSerSerCysThrValAsp 80  
QY 241 CCGGACACCGGTGCTGGCTGCATPAAAGCAATATGGAATATTTGAGTAAATAT 300  
DB 81 ArgAspThrValCysGlyCysArgLysGluMetGlyGlnValGluIleSerSerCysThrValAsp 400  
QY 301 TTCAGTGTCTTCAATTCGAGCTCTGCTCAATGGAACCTTACCTCTCTCTCTCTCTCT 360  
DB 101 PheGlnCysPheAsnCysSerLeuCysLeuAsnGlyThrValHisLeuSerCysGlnGlu 120  
QY 361 AAACAGAACACCGTGTGACCTGCTGATGATGATGATGATGATGATGATGATGATGAT 420  
DB 121 LysGlnAsnThrValCysThrCysHisAlaGlyPhePheLeuArgGluAsnGluCysVal 140  
QY 421 TCCTGTAGTAATCTGAAGAAAGCTGAGTGCAGAGTTGTGCTACCCGATTTGAG 480  
DB 141 SerCysSerAsnCysLysLysSerLeuGluCysThrLysLeuCysLeuProGlnIleGlu 160  
QY 481 AAT 483  
DB 161 Asn 161

## RESULT 4

US-09-899-422-4  
Sequence 4, Application US/09899422  
Patent No. US2002090676A1  
GENERAL INFORMATION:  
APPLICANT: Hauptmann, Rudolph  
APPLICANT: Himmeler, Adolph  
APPLICANT: Maurer, Fredy, Ingrid  
APPLICANT: Stratawa, Christian  
TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for  
TITLE OF INVENTION: Them

FILE REFERENCE: 98,385-H  
CURRENT APPLICATION NUMBER: US/09/899,422  
CURRENT FILING DATE: 2001-08-21  
PRIOR APPLICATION NUMBER: 09/525,998  
PRIOR FILING DATE: 2000-03-15  
PRIOR APPLICATION NUMBER: 08/383,676  
PRIOR FILING DATE: 1998-02-01  
PRIOR APPLICATION NUMBER: 08/153,287  
PRIOR FILING DATE: 1993-11-17  
PRIOR APPLICATION NUMBER: 07/821,750  
PRIOR FILING DATE: 1992-01-02  
PRIOR APPLICATION NUMBER: 07/511,430  
NUMBER OF SEQ ID NOS: 87  
SOFTWARE: Patent In Ver. 2.0  
SEQ ID NO 4  
LENGTH: 161  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-899-422-4

Alignment Scores:  
Pred. No.: 4,398-80 Length: 161  
Score: 941.00 Matches: 161  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 10 Gaps: 0

US-09-882-735-1 (1-483) x US-09-899-422-4 (1-161)

QY 1 GATAGTGTGTGTCCTCCCAAGGAAATATATACACCTCAAAATAATTCGATTGCTGTACC 60  
DB 1 AspSerValCysProGlnGlyLysTyrIleHisProGlnAsnSerIleCysCysThr 20  
QY 61 AAGTCCCAAGGAAACCTATTGTACAAATGACTGTCCAGCCCGGGCGGAGGATACGGAC 120  
DB 21 LysCysHisLysGlyThrTyrLeuTyrAsnAspCysProGlyProGlyGlnAspThrAsp 40  
QY 121 TGCAGGAGTGTGAGAGGCGCTCTTCCACCGCTTCAGAAAACACCTCAGACACTGCTC 180  
DB 41 CysArgGluCysGluSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu 60  
QY 181 AGCTGTCCAAATGCCAAAGAAATGGGTGAGTGGAGATCTCTTTCACAGTGGAC 240  
DB 61 SerCysSerLysCysArgLysGluMetGlyGlnValGluIleSerSerCysThrValAsp 80  
QY 241 CCGGACACCGGTGCTGGCTGCATPAAAGCAATATGGAATATTTGAGTAAATAT 300  
DB 81 ArgAspThrValCysGlyCysArgLysGluMetGlyGlnValGluIleSerSerCysThrValAsp 400  
QY 301 TTCAGTGTCTTCAATTCGAGCTCTGCTCAATGGAACCTTACCTCTCTCTCTCTCTCT 360  
DB 101 PheGlnCysPheAsnCysSerLeuCysLeuAsnGlyThrValHisLeuSerCysGlnGlu 120  
QY 361 AAACAGAACACCGTGTGACCTGCTGATGATGATGATGATGATGATGATGATGATGAT 420  
DB 121 LysGlnAsnThrValCysThrCysHisAlaGlyPhePheLeuArgGluAsnGluCysVal 140  
QY 421 TCCTGTAGTAATCTGAAGAAAGCTGAGTGCAGAGTTGTGCTACCCGATTTGAG 480  
DB 141 SerCysSerAsnCysLysLysSerLeuGluCysThrLysLeuCysLeuProGlnIleGlu 160  
QY 481 AAT 483  
DB 161 Asn 161

## RESULT 5

US-09-907-263-2  
Sequence 2, Application US/09907263  
Patent No. US2002011924A1  
GENERAL INFORMATION:  
APPLICANT: Bendele, Alison M.

Sennello, Regina M.  
Edwards, Carl K.  
TITLE OF INVENTION: COMBINATION THERAPY USING A TNF BINDING  
PROTEIN FOR TREATING TNF-MEDIATED DISEASES  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Amgen Inc.  
STREET: 1840 DeHavilland Drive  
CITY: Thousand Oaks  
STATE: CA  
COUNTRY: US  
ZIP: 91320-1789  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/907,263  
FILING DATE: 17 Jul. 2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 09/326,394  
FILING DATE: 1999-06-04  
APPLICATION NUMBER: US 60/036,355  
FILING DATE: 23-JAN-1997  
APPLICATION NUMBER: US 60/039,315  
FILING DATE: 07 FEB 1997  
APPLICATION NUMBER: US 60/052,023  
FILING DATE: 09-JUL-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Zindrick, Thomas K.  
REGISTRATION NUMBER: 32,185  
REFERENCE/DOCKET NUMBER: A.430D  
INFORMATION PER SEQ ID NO. 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 161 amino acids  
TYPE: amino acid  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO. 2  
US-09-907-263 2  
Alignment Scores:  
Pred. No.: 4.38e-80 Length: 161  
Score: 941.00 Matches: 161  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 10 Gaps: 0  
US-09-882-735 1 (1.483) x US-09-907-263-2 (1-161)  
QY 1 GATAGTGTGTGTCCCAAGAAATATATATCCACCTCAAAATAATTGATTTGCTGTACC 60  
Db 1 AsperterValcysproGlnGlyLysTyrLleHisProGlnAsnAsnSerLleCysCysThr 20  
QY 1 AAGTGTCAAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAA 120  
Db 1 LysCysHisLysGlyThrLysLeuTyrAsnAspCysProGlyProGlyGlnAspThrAsp 40  
QY 1 TCGAGGAGGTGTAAG 180  
Db 1 CysAsnGlyLysLysSerLysSerPheThrAlaSerGlnAsnHisLeuAlaGlyHisLysLeu 60  
QY 1 AAGTGTCAAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAA 240  
Db 1 SerCysSerLysCysArgLysGlnMetGlyGlnValGlnLysSerCysThrValAsp 80  
QY 1 AAGTGTCAAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAA 300  
Db 1 ArgAspThrValCysGlyCysArgLysAsnGlnTyrTrpHisLysTyrTrpSerGlnAsnLeu 100

QY 301 TTCAGTGTCTTAATGTGACGCTCTTGTGCTCATGTGAGACCGTGCACCTCTCTGCGAGAG 360  
Db 101 PheGlnCysPheAsnCysSerLysLeuCysLeuAsnGlyThrValHisLeuSerCysGlnHis 120  
QY 361 AAACAAACACCGCTGTACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGAC 420  
Db 121 LysGlnAsnThrValCysThrCysHisAlaGlyPhePheLeuArgGlnAsnGlnCysVal 140  
QY 421 TCTGTAGTACTGTAAAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480  
Db 141 SerCysSerAsnCysLysLysSerLysLeuGlnCysThrLysLeuCysLeuProGlnLeu 160  
QY 481 AAT 483  
Db 161 Asn 161  
RESULT 6  
US-09-899-429A-6  
Sequence 6, Application US/09899429A  
Patent No. US20020169118A1  
GENERAL INFORMATION:  
APPLICANT: Hauptmann, Rudolph  
APPLICANT: Himmel, Adolph  
APPLICANT: Maurer-Fogy, Ingrid  
APPLICANT: Straszewska, Christian  
TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for  
FILE REFERENCE: 98-385-J  
CURRENT APPLICATION NUMBER: US/09/899,429A  
CURRENT FILING DATE: 2001-07-03  
PRIOR APPLICATION NUMBER: 09/732,356  
PRIOR FILING DATE: 2000-02-23  
PRIOR APPLICATION NUMBER: 08/477,639  
PRIOR FILING DATE: 1995-06-07  
PRIOR APPLICATION NUMBER: 08/383,676  
PRIOR FILING DATE: 1995-02-01  
PRIOR APPLICATION NUMBER: 08/153,287  
PRIOR FILING DATE: 1993-11-17  
PRIOR APPLICATION NUMBER: 07/821,750  
PRIOR FILING DATE: 1992-01-02  
PRIOR APPLICATION NUMBER: 07/511,430  
PRIOR FILING DATE: 1990-04-20  
NUMBER OF SEQ ID NOS: 97  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 6  
LENGTH: 162  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: recombinant  
US-09-899-429A-6  
Alignment Scores:  
Pred. No.: 4.39e-80 Length: 162  
Score: 941.00 Matches: 161  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 9 Gaps: 0  
US-09-882-735 1 (1.483) x US-09-899-429A-6 (1-162)  
QY 1 GATAGTGTGTGTCCCAAGAAATATATATCCACCTCAAAATAATTGATTTGCTGTACC 60  
Db 2 AsperterValcysproGlnGlyLysTyrLleHisProGlnAsnAsnSerLleCysCysThr 21  
QY 61 AAGTGTCAAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAA 120  
Db 22 LysCysHisLysGlyThrLysLeuTyrAsnAspCysProGlyProGlyGlnAspThrAsp 41  
QY 121 TCGAGGAGGTGTAAG 180







; OTHER INFORMATION: Description of Artificial Sequence: recombinant  
 ; OTHER INFORMATION: TNF-BP sequence  
 US-09-899-429A-10

Alignment Scores:  
 Pred. No.: 4-5e-80 Length: 183  
 Score: 941.00 Matches: 161  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 9 Gaps: 0

US-09-882-735-1 (1-483) x US-09-899-429A-10 (1-183)

QY	1	GATAGTGTGTGTCCTCCCAAGSAAATATATATCCACCTCAAAAATAATTCATTTCTGTAAC	60
Db	13	AspSerValCysProGlnGlyLysTyrIleHisProGlnAsnSerIleCysCysThr	32
QY	61	AATGGCCACAAAGAACCTACTTGTACATGACTGTCCAGGCCGGGAGGATACGGAC	120
Db	33	LysCysHisLysGlyThrTyrLeuTyrAsnAspCysProGlyProGlyGlnAspThrAsp	52
QY	121	TGCAGGACACTGTGACAGCGGCTCTTCACGCTTCAGAAACACACCTCAGACACTGCCCTC	180
Db	53	CysArgGluCysGlnSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu	72
QY	181	AGTGTGTCCAAATGGCCAAAGAAATGGGTTCAGTGGAGATCTCTTGTGCACATGGAC	240
Db	73	SerCysSerLysCysArgLysGluMetGlyGlnValIleSerSerCysThrValAsp	92
QY	241	CGGACACCTGTGTGCTGTCAGAGAACCTTCAATGAGTGTCTTGTGCTGCTGCTGCTG	300
Db	93	ArgAspThrValCysGlyCysArgLysGlnSerPheThrAlaSerGluAsnHisLeu	112
QY	301	TTCCAGTGTCTTCAATGAGTGTCTTCAATGAGTGTCTTCAATGAGTGTCTTCAATGAG	360
Db	113	PheGlnCysPheAsnSerLeuCysLeuAsnGlyThrValHisLeuSerCysGlnGlu	132
QY	361	AAACAGAAACCTGTGACAGTGTGACAGTGTGACAGTGTGACAGTGTGACAGTGTGAC	420
Db	133	LysGlnAsnThrValCysThrCysHisAlaGlyPhePheLeuArgGluAsnGlyCysVal	152
QY	421	TCCTGTAGTAATCTGTAGTAATCTGTAGTAATCTGTAGTAATCTGTAGTAATCTGTAG	480
Db	153	SerCysSerAsnSerLysSerLeuGluCysThrLysLeuCysLeuProGlnIleGlu	172
QY	481	AAT 483	
Db	173	Asn 173	

RESULT 11  
 US-09-899-429A-10  
 ; Sequence 10, Application US/09899429A  
 ; Patent No. US20020169118A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Hauptmann, Rudolph  
 ; APPLICANT: Himmler, Adolph  
 ; APPLICANT: Maurer-Pogny, Ingrid  
 ; APPLICANT: Stratowa, Christian  
 ; TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for  
 ; TITLE OF INVENTION: Them  
 ; FILE REFERENCE: 98-385-J  
 ; CURRENT APPLICATION NUMBER: US/09/899,429A  
 ; CURRENT FILING DATE: 2001-07-03  
 ; PRIOR APPLICATION NUMBER: 09/792,356  
 ; PRIOR FILING DATE: 2000-02-23  
 ; PRIOR APPLICATION NUMBER: 08/477,639  
 ; PRIOR FILING DATE: 1995-06-07  
 ; PRIOR APPLICATION NUMBER: 08/183,676  
 ; PRIOR FILING DATE: 1995-02-01  
 ; PRIOR APPLICATION NUMBER: 08/153,287  
 ; PRIOR FILING DATE: 1993-11-17  
 ; PRIOR APPLICATION NUMBER: 07/821,750  
 ; PRIOR FILING DATE: 1992-01-02  
 ; PRIOR APPLICATION NUMBER: 07/511,430  
 ; PRIOR FILING DATE: 1990-04-20  
 ; NUMBER OF SEQ ID NOS: 97  
 ; SOFTWARE: Patent In Ver. 2.0  
 ; SEQ ID NO 10  
 ; LENGTH: 183  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:



Patent No. US20020169118A1  
GENERAL INFORMATION:  
APPLICANT: Hauptmann, Rudolph  
APPLICANT: Himmler, Adolph  
APPLICANT: Maurer-Fogy, Ingrid  
APPLICANT: Stratowa, Christian  
TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for  
FILE REFERENCE: 98-385-J  
CURRENT APPLICATION NUMBER: US/09/899,429A  
PRIOR FILING DATE: 2001-07-03  
PRIOR APPLICATION NUMBER: 09/792,356  
PRIOR FILING DATE: 2000-02-23  
PRIOR APPLICATION NUMBER: 08/477,639  
PRIOR FILING DATE: 1995-06-07  
PRIOR APPLICATION NUMBER: 08/383,676  
PRIOR FILING DATE: 1995-02-01  
PRIOR APPLICATION NUMBER: 08/153,287  
PRIOR FILING DATE: 1993-11-17  
PRIOR APPLICATION NUMBER: 07/821,750  
PRIOR FILING DATE: 1992-01-02  
PRIOR APPLICATION NUMBER: 07/511,430  
PRIOR FILING DATE: 1990-04-20  
NUMBER OF SEQ ID NOS: 97  
SOFTWARE: Patent In Ver. 2.0  
SEQ ID NO 14  
LENGTH: 201  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: recombinant  
OTHER INFORMATION: TNF-BP sequence  
US-09-899-429A-14

Alignment Scores:  
Pred. No.: 4,6e-80 Length: 201  
Score: 941.00 Matches: 161  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 9 Gaps: 0

US-09-882-735-1 (1-483) X US-09-899-429A-14 (1-201)

QY 1 GATAGTGTGTCCTCCCAAGGAAATATATATCCACCTCAAAATAATTCGATTGTGTACC 60  
DB 41 AspSerValCysProGlnGlyIleHisProGlnAsnSerIleCysCysThr 60  
QY 61 AAGTGTCAAAAATAAATAATATGTTGACATGCTCCAGGCGCGGGCAGGATACGGAC 120  
DB 61 LysCysHisGlyThrThrLeuTyrrAsnAspCysProGlyProGlyGlnAspThrAsp 80  
QY 121 TTTACGACCTTTGATAGAGGCTGCTTCTGACCGCTTACAGAAACACCTCAGACACTGCTC 180  
DB 81 CysArgGluCysGluSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu 100  
QY 181 AGTGTGTTAAATATGAAAGAAATATATGAGTGGAGCATCTTTTTCGACAGTGGAC 240  
DB 101 SerCysSerLysCysArgGluMetGlyGlnValGluIleSerSerCysThrValAsp 120  
QY 241 CGGACACCGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 300  
DB 121 ArgAspThrValCysArgGluSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu 140  
QY 301 TTTGACTGTTTAAATGACCTGCTTCTGACCGCTTACAGAAACACCTCAGACACTGCTC 360  
DB 141 PheGlnCysPheAsnGlySerLeuCysLeuAsnGlyThrValHisLeuSerCysGlnGlu 160  
QY 361 AAACAGAAATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420  
DB 161 LysGlnAsnThrValCysThrCysHisAlaGlyPhePheLeuArgGluAsnGluCysVal 180  
QY 421 TCTGTAGTAACTTAAAGAAAGCTGAGTGCATGAAGTTTCTATACATCCCATTTGAG 480

Db 181 SerCysSerAsnCysLysLysSerLeuGluCysThrLysLeuCysLeuProGlnIleVal 200  
QY 481 AAT 483  
Db 201 Asn 201  
RESULT 15  
US-09-899-429A-8  
Sequence 8, Application US/09899429A  
Patent No. US20020169118A1  
GENERAL INFORMATION:  
APPLICANT: Hauptmann, Rudolph  
APPLICANT: Himmler, Adolph  
APPLICANT: Maurer-Fogy, Ingrid  
APPLICANT: Stratowa, Christian  
TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for  
FILE REFERENCE: 98-385-J  
CURRENT APPLICATION NUMBER: US/09/899,429A  
PRIOR FILING DATE: 2001-07-03  
PRIOR APPLICATION NUMBER: 09/792,356  
PRIOR FILING DATE: 2000-02-23  
PRIOR APPLICATION NUMBER: 08/477,639  
PRIOR FILING DATE: 1995-06-07  
PRIOR APPLICATION NUMBER: 08/383,676  
PRIOR FILING DATE: 1995-02-01  
PRIOR APPLICATION NUMBER: 08/153,287  
PRIOR FILING DATE: 1993-11-17  
PRIOR APPLICATION NUMBER: 07/821,750  
PRIOR FILING DATE: 1992-01-02  
PRIOR APPLICATION NUMBER: 07/511,430  
PRIOR FILING DATE: 1990-04-20  
NUMBER OF SEQ ID NOS: 97  
SOFTWARE: Patent In Ver. 2.0  
SEQ ID NO 8  
LENGTH: 211  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: recombinant  
OTHER INFORMATION: TNF-BP sequence  
US-09-899-429A-8

Alignment Scores:  
Pred. No.: 4,65e-80 Length: 211  
Score: 941.00 Matches: 161  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 9 Gaps: 0  
US-09-882-735-1 (1-483) X US-09-899-429A-8 (1-211)  
QY 1 GATAGTGTGTCCTCCCAAGGAAATATATATCCACCTCAAAATAATTCGATTGTGTACC 60  
DB 41 AspSerValCysProGlnGlyIleHisProGlnAsnSerIleCysCysThr 60  
QY 61 AAGTGTCAAAAATAAATAATATGTTGACATGCTCCAGGCGCGGGCAGGATACGGAC 120  
DB 61 LysCysHisGlyThrThrLeuTyrrAsnAspCysProGlyProGlyGlnAspThrAsp 80  
QY 121 TTTACGACCTTTGATAGAGGCTGCTTCTGACCGCTTACAGAAACACCTCAGACACTGCTC 180  
DB 81 CysArgGluCysGluSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu 100  
QY 181 AGTGTGTTAAATGACCTGCTTCTGACCGCTTACAGAAACACCTCAGACACTGCTC 240  
DB 101 SerCysSerLysCysArgGluMetGlyGlnValGluIleSerSerCysThrValAsp 120  
QY 241 CGGACACCGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 300  
DB 121 ArgAspThrValCysArgGluSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu 140  
QY 301 TTTGACTGTTTAAATGACCTGCTTCTGACCGCTTACAGAAACACCTCAGACACTGCTC 360  
DB 141 PheGlnCysPheAsnGlySerLeuCysLeuAsnGlyThrValHisLeuSerCysGlnGlu 160  
QY 361 AAACAGAAATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420  
DB 161 LysGlnAsnThrValCysThrCysHisAlaGlyPhePheLeuArgGluAsnGluCysVal 180  
QY 121 ArgAspThrValCysArgGluSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu 140

Mon Jan 6 08:48:11 2003

us-09-882-735-1.rapb

Page 10

QY 161 TAAAGAGGTTAATTGAGAGCTTAACTTAATGATGAAAGACGGTAACTGTCCTCCGACAGAG 360  
 D6 141 PheGlnGlySerGlnGlySerLeuGlyLeuAlaGlnGlyTyrValHisLeuSerCysGlnGln 160  
 QY 161 AAAAGAAAGAGGCTGCTGACCTGCAATGACGGTTCTTCTTAAAGAGAAACGAGTGTGTC 420  
 D6 161 LysGlnAsnThrValCysThrCysHisAlaGlnPhePheLeuArgLysGlnCysVal 180  
 QY 421 TTTTAAATGATGATTTTAAAGAAAGCTTTAAATGATGATGAAATGTTGATCTTACCCCAATTGAG 480  
 D6 191 SerCysSerGlnGlyLysLysSerLeuGlyCysThrLysLeuGlyLeuProGlnIleGln 200  
 QY 481 AAT 481  
 D6 201 Asn 201

Search completed: January 6, 2003, 03:47:38  
Job time : 33.5 secs



A:Accession: A36555  
 A:Molecule type: mRNA  
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 A:Cross references: CB M3171, NID:9339755, PICH:AAA36754.1; PID:9339756  
 A:Accession: G36555  
 A:Molecule type: protein  
 A:Residues: 39,38,41-53, 'X', 55-79, 'XX', 82-94, 'HW', 'XX', 100-104,107-128,152-167, 'X', 169-2  
 A:Note: The purified protein, called tumor necrosis factor binding protein, is a soluble  
 P:Geyer, P.W.; Barrett, K.; Chantry, D.; Turner, M.; Feldmann, M.  
 Proc. Natl. Acad. Sci. U.S.A. 87, 7380-7384, 1990  
 A:Title: Cloning of human tumor necrosis factor (TNF) receptor cDNA and expression of re  
 A:Reference number: A38281; MUID:9101509; PMID:2170974  
 A:Accession: A38281  
 A:Molecule type: mRNA  
 A:Residues: 1-455 <GRA>  
 A:Cross references: GB:M37764  
 A:Note: The authors translated the codon TGG for residue 371 as Thr, AAG for residue 372  
 R:Kempner, Y.; Kempner, C.; Brakobusch, C.; Engelmann, H.; Zwanz, R.; Adlerka, D.; Holtmann  
 EMBO J. 9, 3269-3278, 1990  
 A:Title: Soluble forms of tumor necrosis factor receptors (TNF-Rs). The cDNA for the typ  
 le form of the receptor.  
 A:Reference number: S12057, MUID:91006021, PMID:1698610  
 A:Accession: S12057  
 A:Molecule type: mRNA  
 A:Residues: 1-455 <NOP>  
 A:Cross references: KXPL:X55313; NID:937223; PID:NCAA9021.1; PID:937224  
 A:Note: parts of soluble TNF binding protein 1, including its amino and carboxyl ends, w  
 R:Kempner, C.; Wallach, D.  
 Gene 134, 209-216, 1993  
 A:Title: Cloning and partial characterization of the promoter for the human p55 tumor ne  
 A:Reference number: J07058, MUID:34085773, PMID:822379  
 A:Accession: J07058  
 A:Molecule type: DNA  
 A:Residues: 1-13 <KEM>  
 R:Seckinger, P.; Vey, E.; Turcatti, G.; Wingfield, P.; Dayer, J.M.  
 Eur. J. Immunol. 20, 1167-1174, 1990  
 A:Title: Tumor necrosis factor inhibitor: purification, NH-2-terminal amino acid sequenc  
 A:Reference number: M60231, MUID:30232116, PMID:2113477  
 A:Accession: M60231  
 A:Molecule type: protein  
 A:Residues: 41-43, 'X', 45-53, 'X', 55-57 <SEC>  
 R:Garganaga, T.; Hwang, C.; Kohr, W.; Cappuccini, F.; Lucchi III, J.A.; Jeffes, E.W.B.; Le  
 Proc. Natl. Acad. Sci. U.S.A. 87, 8781-8784, 1990  
 A:Title: Purification and characterization of an inhibitor (soluble tumor necrosis facto  
 tiens.  
 A:Reference number: A38258, MUID:9102364, PMID:2174164  
 A:Accession: A38258  
 A:Molecule type: protein  
 A:Residues: 41-60 <GAT>  
 A:Experimental source: cancer patient serum  
 R:Olsson, I.; Lantz, M.; Nilsson, E.; Peetre, C.; Thysell, H.; Grubb, A.; Adolf, G.  
 Eur. J. Haematol. 42, 270-275, 1999  
 A:Title: Isolation and characterization of a tumor necrosis factor binding protein from  
 A:Reference number: A60594, MUID:89171156, PMID:2924890  
 A:Accession: A60594  
 A:Molecule type: protein  
 A:Residues: 41-43, 'X', 45-53, 'V', 55-57, 'XX', 60 <OLS>  
 A:Experimental source: renal failure patient urine  
 R:Engelmann, H.; Novick, D.; Wallach, D.  
 J. Biol. Chem. 265, 1531-1536, 1990  
 A:Title: Two tumor necrosis factor-binding proteins purified from human urine. Evidence  
 A:Reference number: A35010, MUID:9010215, PMID:2153136  
 A:Accession: A35010  
 A:Molecule type: protein  
 A:Residues: 41-45 <ENG>  
 A:Experimental source: normal urine  
 R:Kajihara, J.; Asada, A.; Kishihara, S.; Kato, K.  
 Biosci. Biotechnol. Biochem. 58, 226-228, 1994  
 A:Title: Amino acid sequence of natural tumor necrosis factor alpha inhibitor purified f  
 A:Reference number: J02404, MUID:95128033, PMID:7765720  
 A:Accession: J02404  
 A:Molecule type: protein  
 A:Residues: 41-53, 'X', 55-144, 'X', 146-150, 'X', 152-186, 'X', 188-201 <KAU>

A:Experimental source: urine  
 C:Comment: This protein is one of two known receptors for both TNF-alpha (cachectin) and  
 C:Genetics:  
 A:Gene: GDB:TNPRI  
 A:Cross references: GDB:125913; OMIM:191190  
 A:Map position: 12p13.2-12p13.2  
 A:Introns: 13/3; 65/1; 108/1; 158/1; 184/2; 209/1; 247/1; 256/3; 353/1  
 C:Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology  
 C:Keywords: duplication; glycoprotein; receptor; transmembrane protein  
 F:1-11/Domain: signal sequence #status predicted <SIG>  
 F:32-455/Product: tumor necrosis factor receptor 1 #status predicted <MAT>  
 F:30-211/Domain: extracellular #status predicted <EXT>  
 F:41-201/Product: TNF binding protein 1 (tumor necrosis factor alpha inhibitor) #status  
 F:44-82/Domain: NGF receptor repeat homology <NG1>  
 F:84-126/Domain: NGF receptor repeat homology <NG2>  
 F:127-167/Domain: NGF receptor repeat homology <NG3>  
 F:168-196/Domain: NGF receptor repeat homology <NG4>  
 F:232-234/Domain: transmembrane #status predicted <MEM>  
 F:235-455/Domain: intracellular #status predicted <INT>  
 F:54,145,151/Binding site: carboxylate (Asn) (covalent) #status predicted  
 Alignment scores:  
 Pred. No. Length: 455  
 Score: 941.00 Matches: 161  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: Gaps: 0  
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 QY 1 CATAGTGTGTGTCCTCCCAAGAAATATATTCACCTCCAAATTAATTCATTGCTGTAC 60  
 Db 41 AsperValCysProGlnGlnLysTYrLeHisProGlnAsnSerLeIleCysCysThr 60  
 QY 61 AAGGCCCAAGAAAGCACTCTGTAACATGACTGCCAGCGCGGAGGATACGGAC 120  
 Db 61 LysCysHisLysGlnTYrTYrLeuTYrAsnAspCysProGlyProGlyGlnAspThr 80  
 QY 121 TGCAGGAGTGTGAGAGCGGCTCTTACCGCTTCAGAAACACCTGACAGACCTGCTC 180  
 Db 81 CysArgGlnCysGlnSerGlnSerPheThrAlaSerGlnAlaHisLeuArgHisCysLeu 100  
 QY 181 AGCTGCTCCCAATTCCTCAAGAAATGGGTGAGGTGAAATCTTCTTCTTGACAGTGAC 240  
 Db 101 SerCysSerLysCysAspGlnLysCysLeuMetCysGlnValAlaIleSerSerCysThrValAsp 120  
 QY 241 CGGACACCGTGTGTGCTGCTCAGAGAAACAGTACCGGCATTATTGAGTGAATACCTT 300  
 Db 121 ArgAspThrValCysGlnCysArgLysAsnGlnTYrArgHisIleTYrTrpSerGlnAsnLeu 140  
 QY 301 TTCAGTGTCTTCAATTCAGACCTCTGCTCAATGGAGACCGTGCACCTCTCTCCAGAGAG 360  
 Db 141 PheGlnCysPheAsnCysSerLeuCysLeuAsnGlnTYrValHisLeuSerCysGlnGln 160  
 QY 361 AAACAGAACCCGTTGACCTGCTCCATGACAGGTTTCTTAAGCAAAACAGAGTGTCTC 420  
 Db 161 LysGlnAsnThrValCysThrCysHisAlaGlyPhePheLeuArgGlnAsnGlnCysVal 180  
 QY 421 TCCTGTAGTAACTGTAAAGAAACCTGAGTGCACCAAGATTGTGCTTACCCAGATTGAG 480  
 Db 181 SerCysSerAsnCysLysLysSerLeuGlnCysThrTYrLeuCysLeuProGlnIleGln 200  
 QY 481 AAT 483  
 Db 201 Asn 201  
 RESULT 2  
 J04302  
 tumor necrosis factor receptor p55 precursor - pig  
 C:Species: Sus scrofa domestica (domestic pig)  
 C:Date: 29-Nov-1995 #sequence\_\_revision 08-Feb-1996 #text\_\_change 23-Jul-1999  
 C:Accession: J04302; PC4093











Db 207 ThrAsp---CysAspPro 211  
RESULT 9  
B43692  
T2 protein - rabbit fibroma virus  
C:Species: rabbit fibroma virus, Shope fibroma virus  
C:Date: 10-Sep-1993 #sequence\_revision 30 Sep 1993 #text\_change 07-May-1999  
C:Accession: B43692  
R:Upton, C.; DeLange, A.M.; McFadden, G  
Virology 160, 20-30, 1997  
A:Title: Tumorigenic poxviruses: genomic organization and DNA sequence of the telomeric  
A:Reference number: A43692; MUID:87321103; PMID:2820128  
A:Accession: B43692  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-325 <UPT>  
A:Cross references: GB:M17433  
C:Superfamily: myxoma virus T2 protein; NGF receptor repeat homology  
F:64-105/Domain: NGF receptor repeat homology <NG2>  
F:106-147/Domain: NGF receptor repeat homology <NG3>  
Alignment Scores:  
Pred. No.: 2 246-07 Length: 325  
Score: 178.00 Matches: 45  
Percent Similarity: 39.47% Conservative: 15  
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Query Match: 18.92% Indels: 30  
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US 09 882 735-1 (1-483) x B43692 (1-325)  
QY 17 CAATAATTCATTGTTGGTACCAAGTGGACAAAGAACCTACTGTCAATGACTGT 96  
Db 34 GULysAspGlyLeuGlyCysAlaSerCysHisProGlyPheTyrAlaSerArgLeuGly 53  
QY 97 CCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 156  
Db 54 --- GlyProGlySerAsnThrValCysSerProCysGluAspGlyThrPheThrAlaSer 72  
QY 157 GAAACACACCTCAGACACTGGCTTACCTGCG---TCCAAATCCGAAAGAAATGGGTGAC 213  
Db 73 ThrAsnHisAlaProAlaCysValSerCysArgGlyProCysThrGlyHisLeuSer--- 91  
QY 214 GTGAGACTCTCTTTGTACAGTGGACGGACACAGCTGTGGCTGCTGAGGAACACAG 273  
Db 92 ---GluSerGlnProCysAspArgThrHisAspArgValCysAsnCysSerThrGlyAsn 110  
QY 274 TACGGGCAATTATTGACGTCGAAACGCTTTTCCAGTGTCTTCAATTGCGAGCTGCTGCTCAAT 333  
Db 111 TyrCysLeuLeuGlyGlyGlnAsn-----GlyCysArgIleCysAlaPro 125  
QY 334 GGCACGGGAGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 393  
Db 126 GlnThr-----LysCysProAlaGly 132  
QY 394 TTCTTTCTTAAGACAAAGAGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 441  
Db 133 TyrGlyValSerGlyHisThrArgAlaGlyAspThrLeuGlyCysGluLysCysProProHis 152  
QY 442 -----AGCTGCGAGTGCACGAGGAGTGTGC 465  
Db 153 ThrTyrSerAspSerLeuSerProThrGluArgCys 164  
RESULT 10  
A26431  
nervous growth factor precursor, low affinity - rat  
N:Alternate names: NGF receptor  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
C:Accession: A26431; PH1229  
R:Raddeke, M.J.; Misko, T.P.; Hsu, C.; Herzenberg, L.A.; Shooter, E.M.  
Nature 325, 593-597, 1987  
A:Title: Gene transfer and molecular cloning of the rat nerve growth factor receptor.

A:Reference number: A26431; MUID:87115859; PMID:4027580  
A:Accession: A26431  
A:Molecule type: mRNA  
A:Residues: 1-425 <RAD>  
A:Cross references: GB:X05137; NID:G56755; PION:CAA28781.1; PION:G6756  
R:Metsis, M.; Timmus, T.; Allikmets, R.; Saarma, M.; Persson, H.  
Gene 121, 247-254, 1992  
A:Title: Regulatory elements and transcriptional regulation by testis-specific and testis-expressed  
A:Reference number: PH1229; MUID:9307038; PMID:1446821  
A:Accession: PH1229  
A:Molecule type: DNA  
A:Residues: 1-20 <MET>  
A:Cross references: GB:X61269  
C:Comment: This receptor is found on sensory and sympathetic neurons, on neuroblastoma cells  
C:Comment: The cysteine-rich region of the extracellular domain may form part or all of a  
C:Comment: This protein is thought to form a high-affinity receptor when it associates with  
C:Genetics:  
A:Introns: 20/3  
C:Superfamily: nerve growth factor receptor; NGF receptor repeat homology  
C:Keywords: duplication; glycoprotein; heterodimer; monomer; phosphatidylserine receptor;  
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F:30-425/Product: nerve growth factor receptor #status predicted <MAT>  
F:30-251/Domain: extracellular #status predicted <EXT>  
F:33-66/Domain: NGF receptor repeat homology <NG1>  
F:68-109/Domain: NGF receptor repeat homology <NG2>  
F:110-148/Domain: NGF receptor repeat homology <NG3>  
F:150-190/Domain: NGF receptor repeat homology <NG4>  
F:198-249/Region: serine/threonine-rich  
F:252-273/Domain: transmembrane #status predicted <MEM>  
F:274-425/Domain: intracellular #status predicted <INT>  
F:61/Binding site: carbohydrate (Asn) (covalent) #status predicted

Alignment Scores:  
Pred No.: 2 882-07 Length: 424  
Score: 176.50 Matches: 50  
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Best Local Similarity: 30.86% Mismatches: 68  
Query Match: 18.76% Indels: 19  
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US 09 882 735-1 (1-483) x A26431 (1-425)  
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QY 70 AAAGAACTACTTGTCAATGACTGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 129  
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QY 130 TGT---GAGACGGCTCTTCAAGCTTCTTCAAGCAAAATATATATATATATATATATAT 186  
Db 68 CysLeuAspAsnValThrPheSerAspValValSerAlaThrGluProCysLysProCys 87  
QY 187 TCCAAATGCCAAAGCAAAAT 243  
Db 88 ThrGluCys-----LeuGlyLeuGlnSerMetSerAlaProCysValGluAlaAsp 104  
QY 244 GACACCGTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 304  
Db 105 AspAlaValCysArgCys-----AlaTyrGlyTyrTyrGlnAspGluGluThrGly 111  
QY 304 CAGTGTCTTCAATTCAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 460  
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QY 409 ---AACCGAGTGTGTCT 468  
Db 162 ValAspProCysLeuProCysThrValCysGluAspThrGluArgGlnLeuAlaGluCys 181



A>Title: Potential virulence determinants in terminal regions of varicella-zoster virus  
A.Reference number: 220488; MID: J43089747; PMID:18644798  
A.Accession: 128623  
A.Status: preliminary; translated from GR/EMBL/DBR/J  
A.Molecule type: DNA  
A.Molecule residues: 1-348 <MAS>  
A.Cross references: EMBL L22579; MID: J623595; PIDN:AAA60948.1; PIDN:J430107  
A.Experimental source: strain Bangladesh 1975  
C.Superfamily: myxoma virus T2 protein, HGF receptor repeat homology

Alignment Scores:		
Pred. No.:	3.5e-06	Length: 149
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DB:	2	Gaps: 9
US-09-882-735-1 (1-483)	x	T28623 (1-348)

US-09-862-735-1 (1-483) X 12623 (1-348)

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QY	70	AAAGGAACCTACTTGTACAAATGACTCTCCAGCCCGGAGAGATAAGACTAGAGAT	129
Db	48	ProGlyThyThrAlaSerArgLeuCysAspSerLys--ThrAsnThrGlnCysThrPro	66

QY	130	TSISGAGAGGGGCTCTTCACACGCTTACAAAAACATCTAGACACACCTCTCTCAACCTGCTCTC
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QY	190	---AAATGCCGCAAGGAAATGGGTACGTTGAGATCTCTTCTTCACATATGACACGAC:246
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QY	247	ACCGTGTGCTGCTGTGCACCAAGAAACATATAGGCAATTATATGSAATATAAAACCTTTTAA:306

Db	105	ArgIleCysGluCysSerProGlyTyr	-----AATTCACGCTCTGGTCAATGGAATGGCACTCTGG	361
Qy	307	TGCTTC		361
Db	115	CysLeuLeuIlyGlySerGlyCysAlaCysValSerGlnThr		360
Qy	352	TGCCAGGAGAACAGACACACCGGTGTCATTCAGAGTTCTTTTAAAGAAAAA		411
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QY 412 GAGTGTGTCTCC-----TGTAGTAACTGT 434  
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Db 142 ThrSerValGlyAspValIleCysSerProCys 152  
RESULT 15  
D36858  
gene GAP protein - variola virus  
N.Alternate names: B28R protein (COP)  
C.Species: variola virus  
C.Strain: 30 Serp1993  
C.Date: 30 Serp1993  
Accession: D36858

C-Accession: D36858, S46888; S32385, S35987  
 R:Blinov, V. M.  
 Submitted to GenBank, November 1992  
 A:Reference number: A36859  
 A:Accession: D36858  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-349 <BL>  
 A:Cross-references: GB:X69198; MID:Q456758; P11N:CAA49137.1; P11N:4457087  
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R.Kolykhalov, A.A.; Binov, V.M.; Gytarov, V.V.: Pozdnyakov, S.G.; Tikhonov, A. Submitted to the EMBL Data Library, April 1992  
A.Description: Nucleotide sequence analysis of the region of Varicella virus A.Preferred name: S46868  
A.Accession: S46888

A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-349 <KOL>  
A:Cross-references: EMBL:X67117, NID:3517426, FIDR:CAA47640.1, PID:gs16449  
A:Experimental source: strain India-1967, isolate Ind3  
Rashchekunov, S.N.; Blinov, V.M.; Sandakchiev, L.S.  
FBS: Lett. 319, 80-83, 1993  
Article: Genes of varicella and vaccinia viruses necessary to overcome the host protective  
A:Reference number: 31265, XUID:91000261, PMID:8354109  
A:Accession: S12385  
A:Molecule type: DNA  
A:Residues: 31-168 <SHC>  
A:Cross-references: EMBL:X63198  
A:Experimental source: strain India-1967, ssp. major  
C:Genetics:  
A:Gene: 348  
C:Superfamily: myxoma virus T2 protein; NGF receptor repeat homology  
F:32-66/Domain: NGF receptor repeat homology <NGF>  
F:68-108/Domain: NGF receptor repeat homology <NG2>  
F:110-117/Domain: NGF receptor repeat homology <NG3>

## Alignment Scores:

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US-09-882-735-1 (1-483) x D36858 (1-349)

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QY 70 AAAGAAAGCAATCTTAACATGATGATCAAGGACCGGAGGAGGATACGACCTGCAAGGAG 129
   |||
Db 49 ProGlyThrTyrAlaSerArgLeuCysAspSerLys---ThrAsnThrGlnCysThrPro 67
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QY 140 TGTAAAGAGAGTTCCTTAAAGGCTTCAAGAAACCACTCAGACACTGCTCAGCTGCTCC 189
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QY 190 ---AAATGCGGAAAGGAAATGAGTACGATGAGTATCTCTTCTGACATGAGTACCGGAG 246
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Db 88 GlyArgCysAsnSer-----AsnGlnValGlnThrArgSerCysAsnThrThrHisAsn 105
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QY 247 AAGGTGTGTGGTGTGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 306
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Db 106 ArgIleCysGlnCysSerProGlyTyrTyr-----115
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Db 116 CysLeuLeuGlySerSerGlyCysValAlaCysValSerGlnThr-----131
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QY 352 TGGCAGGAAAGAAAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 411
   |||
Db 132 -----LysCysGlyIleGlyTyrGlyValSerGlyHis 142
   |||
QY 412 GASTGTGTCTCC-----TGTAGTAACTGT 435
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Db 143 ThrSerValGlyAspValIleCysSerProCys 153
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Search completed: January 6, 2003, 08:45:50  
Job time : 39 secs



RN [4]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE:91992941, PubMed:1702293;  
 RA Hentler A., Maurer-Pegib I., Kroeke M., Scheuch P., Pitzemaier K.,  
 PA Lantier M., Olsson I., Hauptmann R., Stratowa C., Adolf G.R.;  
 RT "Molecular cloning and expression of human and rat tumor necrosis  
 factor receptor chain (p60) and its soluble derivative, tumor  
 necrosis factor-binding protein.";  
 RL DNA Cell Biol. 9:705-715(1990).  
 PL [5]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Placenta;  
 RX MEDLINE:91017509, PubMed:2170974;  
 RA Gray P.W., Barrett K., Chantry D., Turner M., Feldman M.;  
 RT "Cloning of human tumor necrosis factor (TNF) receptor cDNA and  
 expression of recombinant soluble TNF-binding protein.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 87:7380-7384(1990).  
 RN [6]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE:92550049, PubMed:1151717;  
 RA Fuchs P., Strichl S., Dworzak M., Himmeler A., Ambros P.F.;  
 RT "Structure of the human TNF receptor 1 (p60) gene (TNFR1) and  
 localization to chromosome 12p13.";  
 RL Genomics 13:219-224(1992).  
 RN [7]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Muscle;  
 RX Strausberg R.;  
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
 RN [8]  
 RP SEQUENCE OF 41-45.  
 RX MEDLINE:90110015, PubMed:2153136;  
 RA Engelmann H., Novick D., Malach D.;  
 RT "Two tumor necrosis factor-binding proteins purified from human  
 urine. Evidence for immunological cross-reactivity with cell surface  
 tumor necrosis factor receptors.";  
 RL J. Biol. Chem. 265:1531-1536(1990).  
 RN [9]  
 RP X-RAY CRYSTALLOGRAPHY (2.65 ANGSTROMS) OF 30-211 IN COMPLEX WITH TNFB.  
 RX MEDLINE:93258809, PubMed:8387891;  
 RA Banner D.W., D'Arcy A., Jones W., Gentz P., Schenfeld H.J.,  
 RA Broger C., Loetscher H., Lesslauer W.;  
 RT "Crystal structure of the soluble human 55 kd TNF receptor-human TNF  
 beta complex: implications for TNF receptor activation.";  
 RL Cell 73:431-445(1993).  
 RN [10]  
 RP X-RAY CRYSTALLOGRAPHY (1.85 ANGSTROMS) OF 41-202.  
 RX MEDLINE:97094982, PubMed:8939750;  
 RA Natamath J.H., Devine T.O., Khono H., Sprang S.R.;  
 RT "Structures of the extracellular domain of the type I tumor necrosis  
 factor receptor.";  
 RL Structure 4:1251-1262(1996).  
 RN [11]  
 RP VARIANTS FHF ARG-59; TYR-62; MET-79; PHE-81; ARG-117 AND TYR-117.  
 RX MEDLINE:99215501, PubMed:10199409;  
 RA McDermott M.F., Aksevitjevich I., Galon J., McDermott E.M.,  
 RA Ogunjolaide B.W., Gentola M., Mansfield E., Gadiña M., Karenko L.,  
 RA Petersson T., McCarthy J., Frucht D.M., Aringer M., Torosyan Y.,  
 RA Tepo A.-W., Wilson M., Karaarslan H.M., Wan Y., Todd I., Wood G.,  
 RA Schlimgen R., Kumarajewa T.P., Cooper S.M., Vella J.P., Amos C.I.,  
 RA Mulvey J., Chan K.A., Molloy M.G., Pnaki A., Powell R.J.,  
 RA Hittman G.A., O'Shea J., Kastner D.L.;  
 RT "Germline mutations in the extracellular domains of the 55 kDa TNF  
 receptor, TNFR1, define a family of dominantly inherited  
 autoinflammatory syndromes.";  
 RL Cell 97:133-144(1999).  
 CC FUNCTION: Receptor for TNFSF2/TNF-alpha and homotrimeric  
 TNFSF1/lymphotoxin-alpha. The adaptor molecule FADD recruits  
 caspase 8 to the activated receptor. The resulting death-inducing  
 signaling complex (DISC) performs caspase-8 proteolytic activation  
 which initiates the subsequent cascade of caspases (aspartate-  
 specific cysteine proteases) mediating apoptosis. Contributes to  
 the induction of noncytotoxic TNF effects including anti-viral

CC state and activation of the acid sphingomyelinase.  
 CC -1 SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO  
 CC HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS  
 CC PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY  
 CC WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING  
 CC PROTEINS SUCH AS TRAFs, RIP AND POSSIBLY FADD, ARE RECRUITED TO  
 CC TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX  
 CC ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND  
 CC NF-KAPPA B SIGNALING.  
 CC -1 SUBCELLULAR LOCATION: Type I membrane protein and secreted.  
 CC -1 DOMAIN: THE DOMAIN THAT INDUCES A-SMASE IS PROBABLY IDENTICAL TO  
 CC THE DEATH DOMAIN. THE N-SMASE ACTIVATION DOMAIN (NSD) IS BOTH  
 CC NECESSARY AND SUFFICIENT FOR ACTIVATION OF N-SMASE.  
 CC -1 PTM: The soluble form is produced from the membrane form by  
 CC proteolytic processing.  
 CC DISEASE: Defects in TNFRSF1A are a cause of autosomal dominant  
 CC familial hibernian fever (FHF), a disease characterized by  
 CC recurrent fever, abdominal pain, localized tender skin lesions and  
 CC myalgia.  
 CC -1 SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.  
 CC -1 SIMILARITY: CONTAINS 1 DEATH DOMAIN.  
 CC -1 DATABASE: NAME=PROM; NOTE=CD guide CD120a entry;  
 CC WWW="http://www.ncbi.nlm.nih.gov/row/cd/cd120a.htm".  
 CC -----  
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 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 CC -----  
 CC DR EMBL; X55133; CA93021.1; -;  
 CC DR EMBL; M31294; AAA03210.1; -;  
 CC DR EMBL; M58286; AAA36753.1; -;  
 CC DR EMBL; M63121; AAA36754.1; -;  
 CC DR EMBL; M75866; AAA61201.1; -;  
 CC DR EMBL; M75864; AAA61201.1; JOINED.  
 CC DR EMBL; M73865; AAA61201.1; JOINED.  
 CC DR EMBL; M60275; AAA36756.1; -;  
 CC DR EMBL; A21522; CAA01558.1; -;  
 CC DR EMBL; BC010140; AAH10140.1; -;  
 CC DR PIR; A34899; GQHUT1.  
 CC DR PIR; A35010; A35010.  
 CC DR PIR; S12057; S12057.  
 CC DR PIR; A38208; A38208.  
 CC DR PDB; 1TNR; 31-JUL-94.  
 CC DR PDB; 1NCF; 07-DEC-95.  
 CC DR PDB; 1EXT; 11-JAN-97.  
 CC DR Genew; HGNC:11916; TNFRSF1A.  
 CC DR MIM; 191190; -;  
 CC DR MIM; 142680; -;  
 CC DR InterPro; IPR000488; Death.  
 CC DR InterPro; IPR001368; TNFR\_c6.  
 CC DR Pfam; PF00020; TNFR\_c6; 4.  
 CC DR Pfam; PFC0531; death; 1.  
 CC DR PRODOM; PD000771; TNFR\_c6; 1.  
 CC DR SMART; SM00005; DEATH\_1.  
 CC DR SMART; SM00208; TNFR; 4.  
 CC DR PROSITE; PS00652; TNFR\_NCFR\_1; 3  
 CC DR PROSITE; PS00650; TNFR\_NCFR\_2; 3.  
 CC DR PROSITE; PS00017; DEATH DOMAIN; 1.  
 CC KW Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal;  
 CC Disease mutation; Polymorphism; 3d-structure.  
 CC FT SIGNAL 1 21  
 CC FT CHAIN 22 455  
 CC FT CHAIN 41 291  
 CC FT DOMAIN 22 211  
 CC FT TRASNEM 212 234  
 CC FT DOMAIN 235 455  
 CC FT REPEAT 43 82  
 CC FT REPEAT 83 125  
 CC TNFR-CYS 1.  
 CC TNFR-CYS 2.  
 CC TUMOR NECROSIS FACTOR RECEPTOR  
 CC SUPERFAMILY MEMBER 1A, MEMBRANE FORM.  
 CC TUMOR NECROSIS FACTOR BINDING PROTEIN 1.  
 CC EXTRACELLULAR (POTENTIAL).  
 CC POTENTIAL.  
 CC CYTOPLASMIC (POTENTIAL).  
 CC TNFR-CYS 1.  
 CC TNFR-CYS 2.





FT CARGOHD 54 54 N-LINKED (GLCNAC) (POTENTIAL)  
 FT CARGOHD 86 86 N-LINKED (GLCNAC) (POTENTIAL)  
 FT CARGOHD 145 145 N-LINKED (GLCNAC) (POTENTIAL)  
 FT CARGOHD 151 151 N-LINKED (GLCNAC) (POTENTIAL)  
 SU SEQUENCE 461 AA, 50696 MW, CQ73361E0C99293 CRC64;

Alignment Scores:  
 Pred. No.: 2 54e-57 Length: 461  
 Score: 716.50 Matches: 120  
 Percent Similarity: 85.16% Conservative: 12  
 Best Local Similarity: 77.42% Mismatches: 22  
 Query Match: 76.14% Indels: 1  
 Gaps: 1

US-09-882-735-1 (1-483) x TR1A\_PIG (1-461)

UY 1 GATAGTGTCTCTCCCAAGAAATATATACACCTCAAAATATTCGATTGCTGAC 60  
 DB 41 GUSLELEUCYSPROGILNLYSTYSETHSPROGILNANAGSERILECYGCTHR 60  
 UY 61 AAGIGCCACAAAGAACTACTTGTACATATCTCCUAGCCCGGCGACGATACGAC 120  
 DB 61 LYSCTSH:SLYSGLYTHRTYLEUHSASNPSCYSLGILYPROGILYLEUASPTHRASP 80  
 UY 121 TCCAGGAGTGTGAGAGCGGCTCCCTTCACCGCTTCAGAAACCCCTCAGACACTGCTC 180  
 DB 81 CYSAAGILUCYASPSASGLYTHRPHETHRILASERGLUASNHISLEUTHRGILCYSL 100  
 UY 141 AATCTCTTAAATCTTAAATCTTAAATCTTAAATCTTAAATCTTAAATCTTAAATCTT 240  
 DB 101 SERCYSELTYCYSAISGSEIDMETEERGINALGILLESERPROCYSTRHALASP 120  
 UY 241 CCGAGTAACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300  
 DB 121 AAGAGTCTTAACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 140  
 UY 301 TTTCCAGTCTTCAATTCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360  
 DB 141 PHEGILNCTSLASNGCYSEILEUCYSPROKNGLYTHRTVALGILNLEPROCYSL 160  
 UY 361 AAACAAACACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420  
 DB 161 LYSGLNAPHTLLECYASNTYSHISSEKILYHPHELEUARGASPLYSGLIUCYVAL 180  
 UY 421 TCTCTGATTAATCTTAAAGAAAGCTGAGTGGAGTGGAGTGGAGTGGAGTGGAG 465  
 DB 181 SERCYVALISNGCYSLYASNAIA...ASPCYSLYASNLUCYSL 194

# RESULT 3

TP1A\_MOUSE STANDARD: PRT: 454 AA.

AC P25118;  
 DT 01-MAY-1992 (Rel. 22, Created)  
 DT 01-MAY-1992 (Rel. 22, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Tumor necrosis factor receptor superfamily member 1A precursor (p60)  
 DE (TNF-R1) (TNF-R) (p55).  
 GN TNFRSF1A OP (TNF) OP (TNF-1).  
 OS Mus musculus (Mouse).  
 CC Eukaryota; Metazoa; Chordata; Gnathostomata; Vertebrata; Euteleostomi;  
 CC Eumetazoa; Metazoa; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=9118/885; PubMed=1849278;  
 RA Lewis M., Tartaglia L.A., Lee A., Bennett G.L., Rice G.C.,  
 RA Wang G.H., Chen E.Y., Goeddel D.V.;  
 RA "Cloning and expression of cDNAs for two distinct murine tumor  
 RT necrosis factor receptors demonstrate one receptor is species  
 RT specific";  
 PL Proc. Natl. Acad. Sci. U.S.A. 88:2830-2834(1991).  
 RF [2]  
 RF SEQUENCE FROM N.A.

EX MEDLINE=91246168; PubMed=1645445;  
 RA Goodwin R.G., Anderson D., Jerzy R., Davis T., Brannan C.I.,  
 RA Copeland N.G., Jenkins N.A., Smith C.A.;  
 RT "Molecular cloning and expression of the type 1 and type 2 murine  
 RT receptors for tumor necrosis factor";  
 RT Mol. Cell. Biol. 11:3020-3026(1991).  
 RN [3]  
 RN SEQUENCE FROM N.A.  
 RP MEDLINE=91285014; PubMed=1647956;  
 RA Barrett K., Taylor-Fishwick D.A., Cope A.P., Klesonerhigis A.M.,  
 RA Gray P.W., Feldmann M., Foxwell B.M.J.;  
 RA "Cloning, expression and cross-linking analysis of the murine p55  
 RT tumor necrosis factor receptor";  
 RT Eur. J. Immunol. 21:1649-1656(1991).  
 RN [4]  
 RN SEQUENCE FROM N.A.  
 RP TISSUE=Spleen;  
 PC MEDLINE=92039815; PubMed=1657766;  
 RA Roche J.G., Brockhaus M., Gentz R., Lesslauer W.;  
 RT "Molecular cloning and expression of the mouse Tnf receptor type b.";  
 RT Immunogenetics 34:338-340(1991).  
 RN [5]  
 RN SEQUENCE FROM N.A.  
 RP MEDLINE=94245292; PubMed=8188324;  
 RA Bebo B.F., Linthicum D.S.;  
 RT "Nucleotide sequence of the TNF type I receptor from a mouse  
 RT endothelioma cell line.";  
 RT Immunogenetics 39:450-451(1994).  
 RN [6]  
 RN SEQUENCE FROM N.A.  
 RP MEDLINE=93156721; PubMed=8381516;  
 RA Roche J., Bluetmann H., Gentz R., Lesslauer W., Steinmetz M.;  
 RT "Genomic organization and promoter function of the murine tumor  
 RT necrosis factor receptor beta gene.";  
 RT Mol. Immunol. 30:165-175(1993).  
 RN [7]  
 RN SEQUENCE FROM N.A.  
 RP Strausberg R.;  
 RA Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.  
 RL -1- FUNCTION: Receptor for TNFSF2/TNF-alpha and homotrimeric  
 CC TNFSF1/lymphotoxin-alpha. The adaptor molecule FADD recruits  
 CC caspase-8 to the activated receptor. The resulting death-inducing  
 CC signaling complex (DISC) performs caspase-8 proteolytic activation  
 CC which initiates the subsequent cascade of caspases (apoptate-  
 CC specific cysteine proteases) mediating apoptosis (by similarity).  
 CC -1- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO  
 CC HOMOOLIGERIZATION. ONCE ASSEMBLED THE RECEPTORS DEATH DOMAINS  
 CC PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY  
 CC WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING  
 CC PROTEINS SUCH AS TRAFs, RIP AND POSSIBLY FADD, ARE RECRUITED TO  
 CC TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX  
 CC ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND  
 CC NF-KAPPA B SIGNALING (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -1- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.  
 CC -1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.  
 CC -----  
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 CC -----  
 DR EMBL: M60468; AAA39751.1;  
 DR EMBL: M53377; AAA40464.1;  
 DR EMBL: X59238; AAA4922.1;  
 DR EMBL: X57796; CAA40936.1;  
 DR EMBL: L26349; AAA59361.1;  
 DR EMBL: M76656; AAA40465.1;  
 DR EMBL: M88067; AAA40465.1; JOINED.  
 DR EMBL: M76655; AAA40465.1; JOINED.





DR ProDom; P0000771; TNFR\_c6; 1.  
 DR SMART; SM00005; DEATH; 1.  
 DR PROSITE; PS00208; TNFR; 3.  
 DR PROSITE; PS00652; TNFR\_NGFR\_1; 3.  
 DR PROSITE; PS00050; TNFR\_NGFR\_2; 3.  
 DR PROSITE; PS00017; DEATH\_DOMAIN; 1.  
 DR ProDom; Apoptosis; Transmembrane; Glycoprotein, Repeat; Signal.  
 FT SIGNAL 1 21  
 FT CHAIN 22 461  
 FT  
 FT DOMAIN 22 211  
 FT TRANSMEM 212 234  
 FT DOMAIN 235 461  
 FT REPEAT 43 82  
 FT REPEAT 83 125  
 FT REPEAT 126 166  
 FT REPEAT 167 196  
 FT REPEAT 197 354  
 FT DOMAIN 355 448  
 FT DISULFID 44 58  
 FT DISULFID 59 72  
 FT DISULFID 62 81  
 FT DISULFID 84 99  
 FT DISULFID 102 117  
 FT DISULFID 105 125  
 FT DISULFID 127 143  
 FT DISULFID 146 158  
 FT DISULFID 149 166  
 FT DISULFID 168 179  
 FT DISULFID 182 195  
 FT DISULFID 185 191  
 FT CARBOHYD 54 54  
 FT CARBOHYD 151 151  
 FT CARBOHYD 201 201  
 FT VARIANT 230 230  
 FT  
 FT VARIANT 295 295  
 FT H->P (IN STRAINS LEW/NHSD, ACI/SECHSD,  
 DA/BKL, F344/NHSD AND BN/SSNHSD).  
 SQ SEQUENCE 461 AA; 50669 MW; 883265450FPD22 GPC64;

Alignment Scores:  
 Pred. No.: 5,13e-53 Length: 461  
 Score: 669.00 Matches: 110  
 Percent Similarity: 79.50% Conservative: 18  
 Best Local Similarity: 68.32% Mismatches: 33  
 Query Match: 71.09% Indels: 0  
 Gaps: 0

US 09 882-735-1 (1 481) x TRIA\_RAT (1-461)

QY 1 GATAGTGTGTCTGCTCAAG3AAATATATACCTCTCAAAATATATTCGATTGCTGTACC 60  
 DB 41 AspAsnLeuCysProGlnGlyLysTyrAlaHisProLysAsnAsnSerIleCysCysThr 60  
 QY 61 AAGTGTGACAAAGAACCTACTTGTACAAATGACTGTCTCCAGGCGCGGGGAGGATACGGAC 120  
 DB 61 LysCysHisLysGlyThrTyrLeuValSerAspCysProSerProGlyGlnGluThrVal 80  
 QY 121 TGCAAGAGATGTGTACAGTGGTCTTCAATGCTTCCAGAAACACCACTCAGACACTGCCTC 180  
 DB 81 CysGluValCysAspLysGlyThrThrAlaSerGlnAsnHisValArgGlnCysLeu 100  
 QY 181 AGTGTGTCAATATGTAAGAGAAATATATATATATATATATATATATATATATATATATAT 240  
 DB 101 SerCysLysThrCysArgLysGluMetPheGlnValGluLeuSerProCysLysAlaAsp 120  
 QY 241 CAGTATACCTGT 300  
 DB 121 MetAspThrValCysGlyCysLysLysAsnGlnPheGlnArgTyrLeuSerGluThrHis 140  
 QY 301 TTGAGT 360  
 DB 141 PheGlnCysValAspCysSerProCysPheAsnGlyThrValThrIleProCysLysGlu 160

QY 361 AAACAGAACACCGTGTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTG 420  
 DB 161 LysGlnAsnThrValCysAsnCysHisAlaGlyPhePheLeuSerGlyAsnGluCysThr 180  
 QY 421 TCCTGTACTAATCTAAGAAAGGCTGTGATCTGATCTGATCTGATCTGATCTGATCTGATCTG 480  
 DB 181 ProCysSerHisCysLysLysAsnGlnGluCysMetLysLeuProProValAla 200  
 QY 481 AAT 483  
 DB 201 Asn 201  
 RESULT 6  
 TR23\_MOUSE  
 ID TR23\_MOUSE STANDARD; PET; 176 AA.  
 AC O9ER63; Q8VHC0;  
 DT 15-JUN-2002 (Rel. 41, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Tumor necrosis factor receptor superfamily member 23 (Tumor necrosis  
 factor receptor p60 homolog 1) (TNF receptor family member 23)  
 GN TNFRSF23 OR TNFRSF1A1 OR TNFRH1  
 OS Mus musculus (Mouse)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 PC STRAIN=129/SV; TISSUE=Embryonic stem cells;  
 RX MEDLINE=20519223; PubMed=11063728;  
 RA Engemann S., Stroedicke M., Paulsen M., Franck O., Reinhardt R.,  
 Lane N., Peik W., Walter J;  
 RA "Sequence and functional comparison in the Beckwith-Wiedemann regions;  
 RT implications for a novel imprinting centre and extended imprinting";  
 RT Hum. Mol. Genet. 9:2691-2706(2000).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Fan G., Mao W., Pisser P.;  
 RA "Characterization of SOB, a member of the TNFR family";  
 RL Submitted (JUL-2001) to the EMBL/GenBank/DDRJ databases.  
 CC -1- SUBCELLULAR LOCATION: Type II membrane protein (Potential).  
 CC -1- TISSUE SPECIFICITY: Ubiquitous.  
 CC -1- SIMILARITY: CONTAINS 3 TNFR-CYS REPEATS.  
 CC  
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 DR EMBL; AJ278264; CAC16405.1;  
 DR EMBL; AJ276505; CAC27352.1;  
 DR EMBL; AY046550; AAU05072.1;  
 DR HSSP; P19438; 1EXT.  
 DR MGD; MGI:1930269; Tnfrsf23.  
 DR InterPro; IPR001368; TNFR\_c6.  
 DR Pfam; PF00020; TNFR\_c6; 3.  
 DR SMART; SM00308; TNFR; 3.  
 DR PROSITE; PS00050; TNFR\_NGFR\_2; 2.  
 FW Receptor; Signal anchor; Transmembrane; Glycoprotein; Repeat.  
 FT DOMAIN 1 9 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 10 30 SIGNAL ANCHOR (TYPE 1) MEMBRANE PROTEIN  
 (POTENTIAL).  
 FT DOMAIN 31 176 EXTRACELLULAR (POTENTIAL).  
 FT REPEAT 37 72 TNFR-CYS 1.  
 FT REPEAT 74 114 TNFR-CYS 2.  
 FT REPEAT 115 155 TNFR-CYS 3.  
 FT DISULFID 38 49 BY SIMILARITY.  
 FT DISULFID 50 63 BY SIMILARITY.  
 FT DISULFID 53 72 BY SIMILARITY.









15 JUN 2002 (Rel. 41, Last annotation update)  
DE Tumor necrosis factor receptor superfamily member 3 precursor  
DE (Lymphotxin-beta receptor) (Tumor necrosis factor receptor 2 related  
DE protein) (Tumor necrosis factor receptor)  
GN LTR OR TNFRSF3 OR TNFR  
C5 Homo sapiens (Human)  
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI TaxID=9606;  
RN [1]  
RN FUNCTION  
RP SEQUENCE FROM N.A.  
RC TISSUE=Liver;  
RX MEDLINE=94252381; PubMed=8486360;  
RA Baens M., Chaffanet M., Cassiman J.J., den Berghe H., Marynen P.;  
RT "Construction and evaluation of a hncDNA library of human 12p  
RT transcribed sequences derived from a somatic cell hybrid.";  
RL Genomics 16:214-218(1993).  
RN [2]  
RN SEQUENCE FROM N.A.  
RP TISSUE=Lung;  
RC TISSUE=Lung;  
RA Strausberg R.;  
RT Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RN FUNCTION  
RX MEDLINE=94252209; PubMed=8171123;  
RA Crowe P.D., van Arsdale T.L., Walter R.N., Ware C.F., Hession C.,  
RA Ehrenfels R., Browning J.L., Din W.S., Goodwin R.G., Smith C.A.;  
RT "A lymphotxin-beta-specific receptor.";  
RL Science 264:707-710(1994).  
RN [4]  
RN CHARACTERIZATION  
RX MEDLINE=99223511; PubMed=10207006;  
RA Wu M.-Y., Wang P.-Y., Han S.-H., Hsieh S.-L.;  
RT "The cytoplasmic domain of the lymphotxin beta receptor mediates cell  
RT death in beta cells";  
RL J. Biol. Chem. 274:11868-11873(1999).  
RN [5]  
RN FUNCTION  
RX MEDLINE=20261554; PubMed=10799510;  
RA Rooney I.A., Rutovich K.D., Glass A.A., Borboroglu S., Benedict C.A.,  
RA Whitbeck J.C., Cohen G.H., Eisenberg P.J., Ware C.F.;  
RT "The lymphotxin-beta receptor is necessary and sufficient for  
RT LIGHT mediated apoptosis of tumor cells";  
RL J. Biol. Chem. 275:14307-14315(2000).  
CC [1] FUNCTION: Receptor for the heterotrimeric lymphotxin containing  
CC LTA and LTb, and for TNFSF14/LIGHT. Promotes apoptosis via TRAF3  
CC and TRAF5. May play a role in the development of lymphoid organs  
CC and TRAF5. Self-associates.  
CC [2] SUBUNIT: Self-associates.  
CC [3] SUBCELLULAR LOCATION: Type I membrane protein.  
CC [4] SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.  
CC  
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CC  
CC EMBL: L04270; AAA16757.1;  
CC EMBL: RC056262; AAH26262.1;  
CC HSRP: P25942; ICDP.  
CC Genew: HGNC:6718; LTRR.  
CC MIM: 600979;  
CC InterPro: IPR001368; TNFR\_C6.  
CC Pfam: PF00020; TNFR\_C6; 4.  
CC ProDom: PD000771; TNFR\_C6; 1.  
CC SMART: SM00208; TNFR; 4.  
CC PROSITE: PS00652; TNFR\_NGFR\_1; 2.  
CC PROSITE: PS00656; TNFR\_NGFR\_2; 3.  
CC Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal  
FT SIGNAL 1 30 POTENTIAL.  
FT CHAIN 31 435 TUMOR NECROSIS FACTOR RECEPTOR

FT DOMAIN 31 227 SUPERFAMILY MEMBER 3.  
FT TRANSMEM 228 248 EXTRACELLULAR (POTENTIAL).  
FT DOMAIN 249 435 POTENTIAL.  
FT REPEAT 42 81 CYTOPLASMIC (POTENTIAL).  
FT REPEAT 82 124 TNFR-CYS 1.  
FT REPEAT 125 168 TNFR-CYS 2.  
FT REPEAT 169 211 TNFR-CYS 3.  
FT DISULFID 43 58 TNFR-CYS 4.  
FT DISULFID 59 72 BY SIMILARITY.  
FT DISULFID 62 80 BY SIMILARITY.  
FT DISULFID 83 98 BY SIMILARITY.  
FT DISULFID 101 116 BY SIMILARITY.  
FT DISULFID 104 124 BY SIMILARITY.  
FT DISULFID 126 132 BY SIMILARITY.  
FT DISULFID 139 148 BY SIMILARITY.  
FT DISULFID 142 167 BY SIMILARITY.  
FT DISULFID 170 185 BY SIMILARITY.  
FT CAPROHYD 40 46 N-LINKED (GLCNAC...) (POTENTIAL).  
FT CAPROHYD 177 177 N-LINKED (GLCNAC...) (POTENTIAL).  
SQ SEQUENCE 435 AA; 46709 MW; 62442656026564 CP=64;  
  
Alignment Scores:  
Fred. No.: 2.25e-09 Length: 435  
Score: 187.50 Matches: 49  
Percent Similarity: 44.00% Conservative: 17  
Best Local Similarity: 32.67% Mismatches: 71  
Query Match: 19.93% Indels: 13  
DB: 1 Gaps: 7  
  
US-09-882-735-1 (1-483) x TNFR3\_HUMAN (1-435)  
QY 22 AAATATATCCACCTTCAAAATAATTGATTTCCTTAACTAAATGACACAAACAAATAC H  
Db 49 GluTyrTyrGluProGlnHisArg---IleCysCysSerArgCysProGlyThrTyr 67  
QY 82 TTGTACAAATGACTCTCCAGGCGCGGCGGAGGATAGTACTGAGGAGTGTGAGACGAC 141  
Db 68 ValSerAlaIysCys---SerArgIleArgAspThrValCysAlaThrCysAlaGluAsn 86  
QY 142 TCCCTCACCGGCTTCAGAAACACCACTTAAATCTGCTCACTGCTTCAAAATGCTAAAT 201  
Db 87 SerTyrAsnGluHisTrpAsnTyrLeuThrIleCysGlnLeuCysArgProCysAspPro 106  
QY 202 GAATGGTCTCAGGTGAGATCTCTTCTTCAATGCTGAGGAGGAGGAGGAGGAGGAGGAG 261  
Db 107 ValMetGlyLeuGluGluIleAlaProCysThrSerLysArgIlysthrGluCysAlaCys 176  
QY 262 AGGAGAACCCAGTACCGCGGATATTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 421  
Db 127 GlnProGlyMetPheCysAlaAlaAlaTrpAla-----LeuGluCysThrHisTyrGlu 143  
QY 322 CTC-----TCTCTCAATGAGGAGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 466  
Db 144 LeuLeuSerAspCysProProGlyThrGluAlaGluLeuLysAspGluValGlyGlyGly 164  
QY 367 AACACCGGTGTCACGCT---TGCATGAGAGTCTTTTCTTAAAGAGAGAGAGTCTTTCT 423  
Db 164 AsnAsnHisCysValProCysLysAlaGlyHisPhe-----GlnAsnThrSerSerPro 181  
QY 424 TGTACTAATCTTAAG 453  
Db 182 SerAlaArgCysGlnProHisThrArgCys 191  
  
RESULT 10  
TR16\_HUMAN  
ID TR16\_HUMAN STANDARD; PRT; 427 AA.  
AC P08138;  
DT 01-AUG-1998 (Rel. 08, Created)  
DT 01-AUG-1998 (Rel. 08, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Tumor necrosis factor receptor superfamily member 16 precursor. Low  
DE affinity nerve growth factor receptor (NGF receptor) (Gp160 LINGR)







CC  
DR EMBL: M95181, AAA46632.1, ..  
DR EMBL: AF170726, AAF15046.1, ..  
DR EMBL: AF170726, AAF14887.1, ..  
DR EMBL: A23729, CAA01688.1, ..  
DR PIR: A40566, GQVZML..  
DR InterPro: IFR001368, TNFR\_c6.  
DR Pfam: PF00020, TNFR\_c6; 2..  
DR SMART: SM00208, TNFR\_3.  
DR PROSITE: PS00652, TNFR\_NGFP\_1; 2.  
DR PROSITE: PS00650, TNFR\_NGFP\_2; 2.  
KW Receptor; Glycoprotein; Repeat; Signal.  
FT SIGNAL 1 16  
FT CHAIN 17 326  
FT REPEAT 27 62  
FT REPEAT 63 104  
FT REPEAT 105 147  
FT REPEAT 148 186  
FT DISULFID 28 39  
FT DISULFID 40 53  
FT DISULFID 43 61  
FT DISULFID 64 79  
FT DISULFID 82 96  
FT DISULFID 86 104  
FT DISULFID 106 120  
FT DISULFID 123 146  
FT DISULFID 129 149  
FT DISULFID 164 185  
FT CARBOHYD 66 66  
FT CARBOHYD 181 181  
FT CARBOHYD 205 205  
FT CARBOHYD 238 238  
SQ SEQUENCE 326 AA; 35208 MW; ABBF027E947292FF CRC64;  
  
Alignment Scores:  
Prod. No.: 1.16e-08 Length: 326  
Score: 179.50 Matches: 51  
Percent Similarity: 37.63% Conservative: 19  
Best Local Similarity: 27.42% Mismatches: 47  
Query Match: 19.08% Indels: 49  
Gaps: 7  
  
US 09 882 735-1 (1-483) x VT2\_MXXVL (1-326)  
  
QY 37 CAAATAATTCGATTGTTTATTAATGTTAAAGAACTACTTGTACATGACTGT 96  
Db 34 GLuLYsAspGLyLeuCYsCysThrSerCYsProGLySerTYrAlaSerArgLeuCYs 53  
QY 97 CTAGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 156  
Db 54 --GlyProGlySerAspThrValCYsSerProCYsLysAsnGluThrPheThrAlaSer 72  
QY 157 GAAATACACTAGACACTGCGCTCAGCTGC---TCCAAATGCCGAAAGAAATGGGTCAG 213  
Db 73 ThrAsnHisAlaProAlaCYsValSerTYrArgCYsThrGlyHisLeuSer--- 91  
QY 214 GTGACATCTCTTTTAAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 273  
Db 92 ---GluSerGlnSerCysAspLysThrArgAspArgValCysAspCysSerAlaGlyAsn 110  
QY 274 TAC ..... 276  
Db 111 TyrCysLeuLeuTySGlyGlnGluGlyCysArgGlyCysAlaProLysThrLysCysPro 130  
QY 276 ..... 276  
Db 131 AlaGlyTYrGlyValSerGlyHisThrArgThrGlyAspValLeuCYsThrLysCysPro 150  
QY 277 CGGCATTATTGGAGTGAAGAAACCTTTTCCAGTGTCTTCAATTCAGCTCTGCTCAATGGG 336  
Db 151 ArgTYrThrTYrSerAspAlaValSerSerThrGluThrCYsThrSerSerPheAsnTYr 170

QY 337 ---ACGTTGACCTCTCTCTGAGAGAGAAAAGAAATGCTGTCACCTGACACT 394  
Db 171 HisSerValGluPheAsnLeuTYrProValAsnAspThrSerCYsThrThrAlaGly 190  
QY 394 TTCTTTCTAAGAGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 474  
Db 191 -----ProAsnGluValLysThrSerGluPheSerValThrLeuAsnHis 206  
QY 454 AGGAAGTTGCTGCTACCC 471  
Db 207 ThrAsp---CysAspPro 211  
  
RESULT 14  
VT2\_SFVKA  
ID VT2\_SFVKA STANDARD; PRT; 325 AA.  
AC P25943;  
DT 01-MAY-1992 (Rel. 22, Created)  
DT 01-MAY-1992 (Rel. 22, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Tumor necrosis factor soluble receptor precursor (Protein T2).  
GN T2.  
OS Shope fibroma virus (strain Kasza) (SFV).  
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;  
OC Leporipoxvirus.  
OX NCBI\_TaxID=10272;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=87321103; PubMed=2820128;  
RA Upton C, Delange A M, McFadden G;  
RT "Tumorigenic poxviruses: Genomic organization and DNA sequence of the  
PL telomeric region of the Shope fibroma virus genome.";  
PL Virology 160:20-30(1987).  
RN [2]  
RP FUNCTION  
RX MEDLINE=91207415; PubMed=1850261;  
RA Smith C.A., Davis T., Wignall J.M., Din W.S., Farrah T., Upton C.,  
McFadden G., Goodwin R.G.;  
RT "T2 open reading frame from the Shope fibroma virus encodes a soluble  
form of the TNF receptor";  
PL Biochem. Biophys. Res. Commun. 176:335-342(1991).  
CC 1- FUNCTION: BINDS TO TNF-ALPHA AND BETA. PROBABLY PREVENTS TNF TO  
CC REACH CELLULAR TARGET AND THEREBY DAMPENING THE POTENTIAL.  
CC ANTIVIRAL EFFECTS OF THE CYTOKINE.  
CC 1- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.  
  
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CC or send an email to [license@sib.sib.ch](mailto:license@sib.sib.ch)).  
  
CC EMBL: M17433; .. NOT ANNOTATED CDS.  
DR EMBL: A23727, CAA01687.1, ..  
DR PIR: B43692; B43692.  
DR HSP: P19438; 1EXT.  
DR InterPro: IPR001368, TNFR\_c6.  
DR Pfam: PF00020, TNFR\_c6; 2..  
DR ProDom: PD000771, TNFR\_c6; 1.  
DR SMART: SM00208; TNFR\_3.  
DR PROSITE: PS00652, TNFR\_NGFP\_1; 2.  
DR PROSITE: PS00650, TNFR\_NGFP\_2; 1.  
KW Receptor; Glycoprotein; Repeat; Signal.  
FT SIGNAL 1 16  
FT CHAIN 17 325  
FT REPEAT 27 62  
FT REPEAT 63 104  
FT REPEAT 105 147  
FT REPEAT 148 186  
FT DISULFID 28 39  
FT DISULFID 40 53  
FT BY SIMILARITY.



```
Dh 43 GluSerGluCysProGluGlyGlnHis-----ArgGluGlyGlnPheCysCysGln 59
QY 61 AAGTGGACAAAGAAACCTACTTGTACAATGACTGTCCAGGCGCGGGCGAGATACGGAC 120
Dh 60 ProCysProGluGlyArgLysHisAlaAspCysThrSerProGlyGlyAlaProGln 79
QY 121 TGTACGGAGATTGTACAGGCGG---TCTTTCAACGGCTTCAGAAACCCACCTCAGACACTGC 177
Dh 80 CysValProCysSerGluGlyGluAspTyrThrAspLysAsnHisHisSerSerLysCys 99
QY 178 CTCAGTGTCTCCAAATGCCGAAGGAATGGGTACGTGGAGATCTCTTCTTGACACTG 237
Dh 100 ArgArgCysArgValCysAspGlyGluHisGlyLeuGluValGluLysAsnCysThrArg 119
QY 238 GACCTGTACAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 297
Dh 120 ThrGlnAsnThrLysCysArgCysLysProAsnPhePheCysHis-----ThrSerGln 137
QY 298 CTTTTCACATGTTTAAATTGAGCTTTTGTGTTTAAATGGGACCGTGACCTCTCTCTGCCAG 357
Dh 138 CysGluHisCysAsnProCysThrThrCysGluHisGlyValIleGlu---AsnCysThr 156
QY 358 GACAAACAGACACCGGTGTC 378
Dh 157 ProThrSerAsnThrLysCys 163
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Search completed: January 6, 2003, 03:44:39  
Job time : 28.5 secs





GenCore version 5.1.3  
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OM nucleic protein search, using frame\_plus\_n2p model

Run on: January 6, 2003, 01:17:59 ; Search time 51.5 Seconds  
(without alignments)

3864.884 Million cell updates/sec

Title: US-09-882 735 1

Perfect score: 941

Sequence: 1 qatagtgtgtcccccaagg ..... gctaccacagattgagaat 483

Scoring table: BLOSUM62

Xgapop 10 0, Xgapext 0.5

Xgapop 10 0, Xgapext 0.5

Fgapop 6 0, Fgapext 7.0

Delop 6 0, Delext 7.0

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 1343160

Minimum DR seq length: 0

Maximum DR seq length: 200000000

Post processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

MODEL=frame+.n2p.model -DEV=xih

DR-SPTREMBL 21 -OPMT=fastan -SUFFIX=rspt -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0

UNITS=bits -START=1 -END=1 -MATH=FIX=blosum62 -TRANS=human40.cdi -LIST=45

-DOCCALIGR=200 -THR SCORE=pcr -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL

OUTENT=ptc NPM-ext HPAPX12=500 MINLEN=0 MAXLEN=200000000

USER=US09882735 -ACGN 1 1 19 -runat 03012003 073943 15223 -NCPU=6 -ICPU=3

NO XIPXY NO MMAP LARGQUERY -NEG SCORES=0 -WAIT -LONGLOG -DEV TIMPOUT=120

WARN TIMEOUT=30 -THRFADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPCP=6 -FGAPEXT=7

YGAPOP 10 YGAPEXT=0.5 -DELCP=6 -DELEXT=7

Database :

SPTREMBL 21:\*

1: sp archaea:\*

2: sp bacteria:\*

3: sp fungi:\*

4: sp human:\*

5: sp invertebrate:\*

6: sp mammal:\*

7: sp mhc:\*

8: sp organelle:\*

9: sp phage:\*

10: sp plant:\*

11: sp rodent:\*

12: sp virus:\*

13: sp vertebrate:\*

14: sp unclassified:\*

15: sp rvirus:\*

16: sp bacteriap:\*

17: sp archaeap:\*

Prod. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	740	82.9	446	6 Q95ND3	Q95nd3 felis silve

2	756	80.3	189	6	Q97530	Q97530 canis fami
3	731	77.7	189	6	Q95185	Q95185 felis silve
4	201.5	21.6	413	11	Q90MM1	Q90MM1 mus musculu
5	193	20.5	387	13	Q9PVD4	Q9PVD4 xenopus lae
6	191	20.3	433	11	Q91ZM6	Q91ZM6 rattus norv
7	188	20.0	302	13	Q9PUS0	Q9PUS0 salvelinus
8	182.5	19.4	285	13	Q9DGH7	Q9DGH7 gallus gall
9	179.5	19.1	357	13	Q9NFB4	Q9NFB4 brachydact
10	176.5	18.8	330	12	Q97079	Q97079 cowpox viru
11	176	18.7	459	11	Q62327	Q62327 mus musculu
12	175.5	18.7	312	13	Q9DGH8	Q9DGH8 gallus gall
13	175.5	18.7	322	12	Q92761	Q92761 cowpox viru
14	171.5	18.2	316	12	Q57092	Q57092 ectromelia
15	171.5	18.2	320	12	Q57091	Q57091 ectromelia
16	171.5	18.2	320	12	Q57300	Q57300 ectromelia
17	171.5	18.2	482	11	Q88734	Q88734 mus musculu
18	169	18.0	326	12	Q57120	Q57120 cowpox viru
19	168	17.9	347	12	Q57119	Q57119 cowpox viru
20	168	17.9	351	12	Q57121	Q57121 cowpox viru
21	167.5	17.8	349	12	Q57100	Q57100 monkeypox v
22	167	17.7	326	12	Q57122	Q57122 cowpox viru
23	167	17.7	247	12	Q57115	Q57115 cowpox viru
24	166.5	17.7	349	12	Q57098	Q57098 capripox vi
25	166.5	17.7	349	12	Q57111	Q57111 variola vir
26	166.5	17.7	349	12	Q8UYA7	Q8UYA7 amplex v
27	166.5	17.7	349	12	Q89098	Q89098 variola vir
28	166.5	17.7	349	12	Q57284	Q57284 amplex v
29	166	17.6	360	12	Q57118	Q57118 cowpox viru
30	165	17.5	277	6	Q8MMQ2	Q8MMQ2 ovine aries
31	165	17.5	349	12	Q57109	Q57109 variola vir
32	164.5	17.5	348	12	Q57103	Q57103 monkeypox v
33	164.5	17.5	348	12	Q57108	Q57108 monkeypox v
34	164.5	17.5	348	12	Q57277	Q57277 monkeypox v
35	164	17.4	348	12	Q57112	Q57112 variola vir
36	164	17.4	348	12	Q85407	Q85407 variola vir
37	164	17.4	349	12	Q57110	Q57110 variola vir
38	164	17.4	349	12	Q95118	Q95118 variola vir
39	164	17.4	351	12	Q71559	Q71559 cowpox viru
40	162.5	17.3	349	12	Q57092	Q57092 monkeypox v
41	162.5	17.3	349	12	Q57121	Q57121 monkeypox v
42	162.5	17.3	349	12	Q57102	Q57102 monkeypox v
43	162.5	17.3	349	12	Q57291	Q57291 monkeypox v
44	162	17.2	349	12	Q57305	Q57305 cowpox viru
45	162	17.2	350	12	Q57123	Q57123 cowpox viru

## ALIGNMENTS

RESULT 1

Q95ND3 ID Q95ND3 PRELIMINARY; PRT; 446 AA.

AC Q95ND3; 01-DEC-2001 (TREMREL. 19, Created)

DT 01-DEC-2001 (TREMREL. 19, Last sequence update)

DT 01-MAR-2002 (TREMREL. 20, Last annotation update)

DE Tumor necrosis factor type 1.

GN TNFR I.

OS Felis silvestris catus (Cat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Carnivora; Fissipedia, Felidae; Felis.

OX NCBI\_TaxID=9685;

RN [1]

RP SEQUENCE FROM N A.

PA Mizuno T., Goto Y., Raba K., Masuda K., Ohno K., Trajimoto H.;

PT "Molecular cloning of feline tumor necrosis factor receptor type 1

RT (TNFR I) and expression of TNFR I and TNFR II in various disease in

RT cats.";

RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AB051103; BAB55455.1; -

DR InterPro; IPR000345; CytC\_heme\_bind.

DR InterPro; IPR000488; Death.

DR InterPro; IPR000561; EGF-like.

DR InterPro; IPR001368; TNFR\_c6.



DR EMBL; U72144; AAB95089.1; 1.  
 DR HSSP; P19438; LEXT.  
 DR InterPro; IPR000561; EGF-like.  
 DR InterPro; IPR001368; TNFR\_c6.  
 DR Pfam; PF00020; TNFR\_c6; 3.  
 DR SMART; SM00208; TNFR; 1.  
 DR PROSITE; PS01186; EGF\_2; UNKNOWN 1.  
 DR PROSITE; PS00652; TNFR\_NGFR\_1; 3.  
 DR PROSITE; PS00350; TNFR\_NGFR\_2; 3.  
 KW Receptor.  
 FT NON TER 189 189  
 SQ SEQUENCE 189 AA; 21420 MW; F3FBCE809D7DBE CRC64;  
 Alignment Scores:  
 Pred. No.: 1,95e-66 Length: 189  
 Score: 731.00 Matches: 124  
 Percent Similarity: 91.03% Conservative: 8  
 Best Local Similarity: 85.52% Mismatches: 13  
 Query Match: 77.68% Indels: 0  
 DB: 6 Gaps: 0  
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 QY 10 TGTGCTAAAGAAATATATACACCTCAAAATAATTCGATTCTCTACCAAGTCCAC 69  
 Db 44 CysProGlnGlyLysTyrHisProGlnAspAsnSerIleCysCysThrLysCysHis 63  
 QY 70 AAGGAACCTACTGTGACAAATGACTGTCCAGCGCGCGGAGGATACGAGTACGAGGAG 129  
 Db 64 LysGlyThrTyrLeuTyrAsnAspCysGluGlyProGlyLeuAspThrAspCysArgGlu 83  
 QY 110 TGTGACATGCTGTTTACGCTTTCAGAGTTTCAGAAACCACTCAGACTCCCTGCTCC 189  
 Db 84 CysGluAsnGlyThrPheThrAlaSerGluAsnTyrLeuArgGlnCysLeuSerCysSer 103  
 QY 130 AATGCTGAAATGAAATGCTTATGCTGATCTTCTGACAGTGGACGAGGACAC 249  
 Db 104 LysCysArgLysGluMetTyrGlnValGlnLeuSerProCysThrValTyrArgAspThr 123  
 QY 258 GTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 309  
 Db 124 ValCysGlyCysArgLysAsnGlnTyrArgTyrTyrTrpSerGluThrHisPheGlnCys 143  
 QY 310 TGCATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 369  
 Db 144 LeuAsnCysSerLeuCysLeuAsnGlyThrValGlnLeuSerCysLysGluThrGlnAsn 163  
 QY 378 AGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 429  
 Db 164 ThrValCysThrCysHisAlaGlyPhePheLeuArgGlyAsnGluCysValSerCysVal 183  
 QY 430 AACTGTAAGAAAGC 444  
 Db 184 AmCysLysLysAsn 188  
 RESULT 4  
 Q95MM1  
 ID Q95MM1 PRELIMINARY; PRT; 413 AA.  
 AC Q95MM1;  
 FT 01-JUN 2001 (TrEMBLrel. 17, Created)  
 DT 01-JUN 2001 (TrEMBLrel. 17, Last sequence update)  
 DT 01-JUN 2002 (TrEMBLrel. 21, Last annotation update)  
 DE WSL\_1-like protein.  
 GN TNFRSP12.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Euthetia; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=129/SV;  
 RX MEDLINE=21158184; PubMed=11261933;  
 RA Wadd E.C.Y., Kitson J., Thern A., Williamson J., Farrow S.N.,

RA Owen M.J.;  
 RT "Genomic structure, expression, and chromosome mapping of the mouse  
 RT homologue for the WSL-1 (DR3, Apo3, TRAMP, LARD, TR3, TNFRSP12)  
 RT gene".  
 RL Immunogenetics 53:59-63(2001).  
 DP EMBL; AF129969; AAF11256.1; 1.  
 DR HSSP; F25942; ICDF.  
 DR MGD; MGI:1934667; Tnfrsf12.  
 DR InterPro; IPR000488; Death.  
 DR InterPro; IPR000561; EGF-like.  
 DR InterPro; IPR001368; TNFR\_c6.  
 DR Pfam; PF00531; death; 1.  
 DR Pfam; PF00020; TNFR\_c6; 3.  
 DR SMART; SM00005; DEATH; 1.  
 DR SMART; SM00208; TNFR; 3.  
 DR PROSITE; PS00017; DEATH DOMAIN; 1.  
 DR PROSITE; PS01186; EGF\_2; UNKNOWN 1.  
 DR PROSITE; PS00652; TNFR\_NGFR\_1; UNKNOWN 1.  
 DP PROSITE; PS00050; TNFR\_NGFR\_2; 1.  
 SQ SEQUENCE 413 AA; 44453 MW; 69F21B85D0DABAF CRC64;

## Alignment Scores:

Pred. No.: 2,95e-12 Length: 413  
 Score: 203.50 Matches: 51  
 Percent Similarity: 44.87% Conservative: 19  
 Best Local Similarity: 32.69% Mismatches: 54  
 Query Match: 21.63% Indels: 32  
 DB: 11 Gaps: 7

US-09-882-735-1 (1-483) x Q99MM1 (1-413)

QY 52 TGTGTACCAAGTGCATACAAAGAAATATATATATATATATATATATATATATATATATAT 111  
 Db 54 CysCysArgGlyCysProLysGlyHisTyrMetLysAlaProCysAlaLubProCysHis 74  
 QY 112 GATACGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 171  
 Db 74 AsnSerThrCysLeuProCysProSerAspThrPheLeuThrArgAspAsnHisHis 94  
 QY 172 ---CACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 239  
 Db 94 ThrAspCysThrArgCysGlnValCysAspGluGluAlaLeuGlnValThrLeuGluAsn 114  
 QY 229 TGCACATGACACCGCGGACATCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 289  
 Db 114 CysSerAlaLysSerAspThrHisCysGlyCysGlnSerGly 128  
 QY 289 AGTCAGAAACCTTTTCCAGTGTCTCAATTCAGCTCTCTGCTCAATCGCA 307  
 Db 129 ---CysValAspCysSerThrValProCysGlyLysSerSerPro 149  
 QY 338 ---CCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 408  
 Db 142 oPheSerCysValProCysGlyAlaThrThrProValHisGluAlaProThrPro Arg 161  
 QY 379 ACCTGCGCATGCAAGTCTTTCTTTTAAAGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAG 429  
 Db 162 ProCysLeuProGlyPheTyrIleArgGlyAsnAspCysThrSerCysProThrGlyPhe 181  
 QY 427 ---AGTAACGTGAAGAAAGCTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 465  
 Db 182 SerSerValCysProLysAla CysThrAlaValCys 193  
 RESULT 5  
 Q9PVD4  
 ID Q9PVD4 PRELIMINARY; PRT; 387 AA.  
 AC Q9PVD4;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
 DE P75-like transmembrane protein fullback.  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

CC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;  
 CC Xenopus; Xenopus  
 OK NCBI\_TaxID:8355;  
 RN [1]  
 RE SEQUENCE FROM N.A.  
 RA Hick E., Sun B.T., Collins-Racie L., Lavallie E., Sive H.L.;  
 RT "Identification and Characterization of fullback, a Novel Posteriorly-  
 RT Expressed Xenopus Gene";  
 RT Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF131890; AAB54072.1; -  
 DR HSSP; P07174; INCR.  
 DR InterPro; IPR001083; Copper-fist.  
 DR InterPro; IPR000488; Death.  
 DR InterPro; IPR001368; TNF\_c6.  
 DR Pfam; PF00531; death; 1.  
 DR Pfam; PF00020; TNF\_c6; 4.  
 DR SMART; SM00412; Cu\_F1SF; 1.  
 DR SMART; SM00005; DEATH; 1.  
 DR JMat; JMat013; TNF; 4.  
 DR PROSITE; PS00017; TRAF\_TKMAIN; 1  
 DR PROSITE; PS00652; TNFR\_NGFR\_1; UNKNOWN\_3.  
 DR PROSITE; PS00652; TNFR\_NGFR\_2; 4  
 DR PROSITE; PS00652; TNFR\_NGFR\_3; 4  
 DR Transmembrane.  
 KW Transmembrane.  
 SQ SEQUENCE 387 AA, 42066 MW, 1A386A239C7C8A82 CRC64;

Alignment Scores:  
 Pred. No.: 3.5e-12 Length: 387  
 Score: 193.00 Matches: 53  
 Percent Similarity: 46.39% Conservative: 24  
 Best Local Similarity: 31.93% Mismatches: 71  
 Query Match: 20.51% Indels: 18  
 DB: Gaps: 10

US-09-882-735-1 (1-483) x Q9PVT4 (1-387)

QY 1 GATAGTGTGTCCTCCCAAGAAATATATCCACCCCTCAAAATATGATTTGCTGAC 60  
 DB 22 GUAAPVALCYSGLSERGLYLEUTY-----THYNSERGLYLSYCSYSSER 38  
 QY 61 AAGTCCCAAAAGAAATATATGATTTGCTGACCTGACGAGATGAC 120  
 DB 39 LEUCYSPVALAGLYPHEGLYVALVALPROCY-----GLYASPERASPHLYS 56  
 QY 141 TCCAGAGAGATGTTTCAATGCTGACCTGACGAGATGCTGCTTGGACACTGC 177  
 DB 57 CYSGLSERGLYLSYCSYSSERGLYLSYCSYSSERGLYLSYCSYSSER 76  
 QY 178 TCCAGAGAGATGTTTCAATGCTGACCTGACGAGATGCTGCTTGGACACTGC 237  
 DB 77 GINPROCYSPHATINCYSGLSERPROSELEUTHILEUGIN---SERANCYSTHARG 95  
 QY 238 TCCAGAGAGATGTTTCAATGCTGACCTGACGAGATGCTGCTTGGACACTGC 297  
 DB 96 GUGINASPHTHVALCYSAIGYSPHGLIARGINTYLYEASR-----SERANGLY 113  
 QY 298 GTTTCAGAGATGTTTCAATGCTGACCTGACGAGATGCTGCTTGGACACTGC 354  
 DB 114 TTT-----CYSGLSERGLYLSYCSYSSERGLYLSYCSYSSERGLYLSYCSYSSER 131  
 QY 355 CAGAGAGAGATGTTTCAATGCTGACCTGACGAGATGCTGCTTGGACACTGC 405  
 DB 132 THHISANLYSANTHVALCYSGLSERGLYLSYCSYSSERGLYLSYCSYSSER 151  
 QY 406 -----GAGAGAGATGTTTCAATGCTGACCTGACGAGATGCTGCTTGGACACTGC 456  
 DB 152 SERISERGLYSPHATINCYSGLSERGLYLSYCSYSSERGLYLSYCSYSSER 171  
 QY 457 AAGTCCCAAAAGAAATATATGATTTGCTGACCTGACGAGATGAC 474  
 DB 172 GLYAPVALPROGIN 177

RESULT 6  
 Q912M6

ID Q912M6 PRELIMINARY; PRT; 433 AA.  
 AC Q912M6;  
 DT 01-DEC-2001 (TREMBlrel. 19, Created)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)  
 DE Tumor necrosis factor receptor type II (fragment).  
 OS Rattus norvegicus (Rat).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OK NCBI\_TaxID=10116;  
 RN [1]  
 RE SEQUENCE FROM N.A.  
 RC STRAIN=SPRAGUE-DAWLEY;  
 RA Osburn B., Peiser C., Doemling D., Schomburg L., Voigt K., Bickel U.;  
 RT "TNF-receptors p60 and p80 are constitutively expressed by rat brain  
 RT capillary endothelial cells and participate in TNF-alpha transport  
 RT through the blood-brain barrier";  
 RT Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF420214; AAL16021.1; -  
 DR InterPro; IPR001368; TNFR\_c6.  
 DR Pfam; PF00020; TNFR\_c6; 4.  
 DR PROSITE; PS00652; TNFR\_NGFR\_1; UNKNOWN\_2.  
 DR PROSITE; PS00652; TNFR\_NGFR\_2; 3.  
 KW Receptor.  
 KW NON\_TER.  
 FT NON\_TER 1  
 FT NON\_TER 433  
 SQ SEQUENCE 433 AA, 45723 MW, 75736D835E72CA4A CRC64,

Alignment Scores:  
 Pred. No.: 5.63e-11 Length: 433  
 Score: 191.00 Matches: 52  
 Percent Similarity: 44.03% Conservative: 18  
 Best Local Similarity: 32.70% Mismatches: 79  
 Query Match: 20.30% Indels: 10  
 DB: Gaps: 7

US-09-882-735-1 (1-483) x Q912M6 (1-433)

QY 10 TGTCCCAAGAAATATATCCACCCCTCAAAATATGATTTGCTGACGAGTCCAC 69  
 DB 20 CYSGINLESEGLINGLYTYRTPYSLYSLYSLAGLMETCYSLALYSCYSPRO 39  
 QY 70 AAGAGACTGCTGATGACGATGCTGACGAGTCCAGAGATGCTGACGAGTCCAG 129  
 DB 40 PROGLINGLYTALYSLYSHISNECY-----ASYLTYTHSERASPHRYALYSLALAP 58  
 QY 130 TGTAGAGAGTCTGCTGACGAGTCCAGAGATGCTGCTTGGACACTGCCTGAGTGC 186  
 DB 59 GYSLALAGLYMETPHEHTHGINVALTPRASNHILEUHNISHTHCYSEUSERCYSER 78  
 QY 187 TCCAAATGCGGAAAGAAATGAGTCCAGAGATGCTGCTTGGACACTGCCTGAGTGC 246  
 DB 79 SERISERGLYSPHATINCYSGLSERGLYLSYCSYSSERGLYLSYCSYSSER 96  
 QY 247 ACCGTGTGAGTCCAGAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGT 300  
 DB 97 ARGVALCYSLALCYSAANALAPSERTYRGLYALILEUHLISERGLYLSYCSYSSER 116  
 QY 301 TTCAGAGTCTCAATGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 357  
 DB 117 ARGINCYSMETCYSLYSEUSERLYSGYLPYGLYPHEGLYVALVALARGSERARGTHR 136  
 QY 358 GAGAAAG 414  
 DB 137 SERANGLYSHVALILECYSEALALCYSAALAPROGLYTHPHE-----SERISPHR 154  
 QY 415 TGTGTCCTGCTGATGACCTGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGT 471  
 DB 155 THRSERTHIRAPVALCYSAIRPROHISARGILECYSERILEUHLALALPRO 173

RESULT 7  
 Q9PUS0 PRELIMINARY; PRT; 302 AA.

Q9PUS0;  
 DT 01-MAY-2000 (Tremblrel. 13, Created)  
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)  
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)  
 DE Decoy TNF receptor.  
 OS Salvelinus fontinalis (Brook trout) (Brook char).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Salvelinus.  
 OX NCBI\_TaxID=8038;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20111091; PubMed=10642582;  
 RA Robe J., Goetz F.W.;  
 RT "A tumor necrosis factor decoy receptor homologue is up-regulated in  
 RT the brook trout (Salvelinus fontinalis) ovary at the completion of  
 RT ovulation."  
 RL Biol. Reprod. 62:420-426(2000)  
 DR EMBL; AF156738; AAD56428.1; -  
 DR HSP; O14763; IDAV.  
 DR InterPro; IPR000561; EGF-like  
 DR InterPro; IPR001368; TNFR\_C6  
 DR Pfam; PF00020; TNFR\_C6; 4  
 DR SMART; SM00208; TNFR; 4  
 DR PROSITE; PS01186; EGF\_2; UNKNOWN\_1  
 DR PROSITE; PS00652; TNFR\_NGFR\_1; UNKNOWN\_1  
 DR PROSITE; PS00650; TNFR\_NGFR\_2; 1.  
 KW Receptor.  
 SQ SEQUENCE 302 AA; 34017 MW; E44C73477F05C3DF CRC64;  
 Alignment Scores:  
 Pred. No.: 1,11e-10 Length: 302  
 Score: 188.00 Matches: 45  
 Percent Similarity: 46.15% Conservative: 21  
 Best Local Similarity: 31.47% Mismatches: 53  
 Query Match: 19.98% Indels: 24  
 DB: 13 Gaps: 7  
 US-09-882-735-1 (1-483) X Q9PUS0 (1-302)  
 QY 46 TCGATTCTCTTCACTAAATGTCACAAAGGAAAGTACTTGTACATGACTGTCAGGCGCG 105  
 DB 33 SerIleValCysAspArgCysProGlyThrTyrLeuArgAlaProCysSerAlaMet 52  
 QY 106 GAGCAGATACGAGTCTTACAGGAGTGTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 165  
 DB 53 ...AlaGlySerAspCysAlaValCysProAsnGlyAlaTyrThrGluPheTrpAsnHis 71  
 QY 166 CTCAGACACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 225  
 DB 72 IleSerLysCysLeuArgCysSerMetCysAlaGlu-----AsnGlnValValLysGln 89  
 QY 226 TTTTTCACACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 285  
 DB 90 GluCysSerProSerAsnAsnCysGluCysGluCysGluCysLysGluGly-----TyrTyr 106  
 QY 286 TCGAGTAAAGATTTTTCAGTAAATTCAGTAAATTCAGTAAATTCAGTAAATTCAGTAAATTC 327  
 DB 107 PheAsnLysLysTyrGluAlaCysIleLysHisLysGluCysProGlyTyrGlyAla 126  
 QY 328 --CTAATGCAATCTTCACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 381  
 DB 127 AsnThrThrGlyThrProHis-----GlnAspThrGluCysValGln 140  
 QY 382 TGCATGCAAGTTTCTTCTAGAGAAACAGAG-----TGTGCTCTCTCTGAGT 429  
 DB 141 CysGlnAlaGlyPheTyrSerGluValSerSerAlaLysAlaThrCysLeuAlaGlnSer 160  
 QY 430 AACTGTAG 438  
 DB 161 AsnCysLys 163  
 RESULT 8

Q9DGH7  
 ID Q9DGH7 PRELIMINARY; PRT; 285 AA.  
 AC Q9DGH7;  
 DT 01-MAR-2001 (Tremblrel. 16, Created)  
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)  
 DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)  
 DE Fas ligand receptor soluble form (Fragment).  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OX NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX Bridgman J.T., Johnson A.L.;  
 RT "Fas Expression and Regulation in Hen Granulosa Cells";  
 RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF346475; AAG32243.1; -  
 DR HSP; O14763; IDAV.  
 DR InterPro; IPR000488; Death.  
 DR InterPro; IPR001368; TNFR\_C6.  
 DR Pfam; PF00531; death\_1  
 DR Pfam; PF00020; TNFR\_C6; 2  
 DR SMART; SM00005; DEATH; 1.  
 DR SMART; SM00208; TNFR; 2.  
 DR PROSITE; PS00017; DEATH DOMAIN; 1  
 DR PROSITE; PS00652; TNFR\_NGFR\_1; UNKNOWN\_1  
 DR PROSITE; PS00050; TNFR\_NGFR\_2; 2.  
 KW Receptor.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 285 AA; 32431 MW; A9761960CDD70E6D CRC64;  
 Alignment Scores:  
 Pred. No.: 4.04e-10 Length: 285  
 Score: 182.50 Matches: 36  
 Percent Similarity: 46.36% Conservative: 15  
 Best Local Similarity: 32.73% Mismatches: 54  
 Query Match: 19.39% Indels: 5  
 DB: 13 Gaps: 3  
 US-09-882-735-1 (1-483) X Q9DGH7 (1-285)  
 QY 52 TCGTGTACAGTCCACCAAGGAAAGTACTTGTACATGACTGTCAGGCGCGAG 111  
 DB 6 CysCysThrLysCysLysArgGlyHisValLysSerIleAspCysProLysThrGlnIle 26  
 QY 112 GATACGAGTCTGAGGAGTGTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 169  
 DB 26 -----HisCysValProCysLysCysGlyGluGluTyrMetAspHisIleAsnAspLeu 43  
 QY 169 AGACACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 228  
 DB 44 AspGluCysMetArgCysArgSerCysAspLysAlaLeuGlyLeuGluValValLysAsn 63  
 QY 229 TGCACAGTGGACCGGACACCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 288  
 DB 64 CysThrSerThrGluAsnAlaGluCysSerCysAlaLysAsnHisTyrCysAsn 81  
 QY 289 AGTGAAGAACTTTTCCAGTCTGCTTCAATTCAGTCTGCTTCAATTCAGTCTGCTTCAATTC 348  
 DB 82 SerSerArgCysGluHisCysGluSerCysThrValLysGluAsnGlyGlnIleGlyLys 101  
 QY 349 TCTGTCAGGAGAAACACACACCGCTTTC 378  
 DB 102 GluCysThrSerThrSerAspThrValCys 111  
 RESULT 9  
 Q9DF34  
 ID Q9DF34 PRELIMINARY; PRT; 357 AA.  
 AC Q9DF34;  
 DT 01-MAR-2001 (Tremblrel. 16, Created)  
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)  
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)



Best Local Similarity: 27.81% Mismatches: 62  
Query Match: 18.76% Indels: 25  
Gaps: 6

US 09-882-735-1 (1-483) x 057079 (1-320)

QY 40 AATAATGCGATTGTTGTTTACCAAGTGGCCAAAGGAACTACTTGTACAAATGACTGTCCA 99  
DB 38 SerAsnAsnLeuCysCysLysGlnCysAspProGlyMetTyrMetThrHisSerCys... 56  
QY 100 GACGCGGCGGAGATACGAGTGCAGGAGTGTGAGACGCGCTCTTCACCGCTTCAGAA 159  
DB 57 AsnThrThrSerAsnThrLysCysAspLysCysProAspGlyThrPheThrSerIlePro 76  
QY 160 AATCACTTAT 216  
DB 77 AsnHisIleProThrCysLeuSerCysArgGlyLysCys-----SerSerAsnHisVal 94  
QY 217 GACATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 276  
DB 95 GluThrLysSerCysSerAsnThrGlnAspArgValCysValCysAlaSerGlyTyrTyr 114  
QY 279 CAGCATATGCGAGTCAAAACCTTTTTCAGTGTTCATATTCAGCCCTGCTCAATGGG 336  
DB 115 CysGluPheGluGlySerAsn-----GlyCysArgGlyCysValProSln 129  
QY 337 ACGTGCACCT 396  
DB 130 Thr-----LysCysAspSerGlyTyr 136  
QY 397 TTCTTA-----AGAGAAAGTATGTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 447  
DB 137 GlyValTyrGlyTyrSerSerLysGlyAspValIleCysLysLysCysProGlyAsnIle 156  
QY 448 GATGTGACCAATTTGTGCTATCCCGCATGATGAG 480  
DB 157 AspLysCysAspLeuSerPheAsnSerIleAsp 167

RESULT 11

Q62327 PRELIMINARY; PRT; 459 AA  
AC Q62327;  
DT 01 NOV-1996 (TREMURel. 01, Created)  
DT 01 NOV-1996 (TREMURel. 01, Last sequence update)  
DE 01-JUN-2002 (TREMURel. 21, Last annotation update)  
DE Murine tumor necrosis factor receptor 2 protein (Fragment).  
GN TNFRSF1B.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID:10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN:MO;  
RA Powell E.E., Wicker L.S., Peterson L.R., Todd J.A.;  
RT "Amino acid variation in the tumor necrosis factor receptor 2 is  
linked to autoimmune diabetes in NOD mice.";  
RL Genomics 0:0-0(0).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN:MO;  
RX MEDLINE-95178848; PubMed-7873884;  
RA Powell E.E., Wicker L.S., Peterson L.R., Todd J.A.;  
RT "Allelic variation of the type 2 tumor necrosis factor receptor  
gene.";  
RL Mamm Genome 5:726-727(1994)  
DR EMBL; X76401; CAA53981.1; ..  
DR HSSP; P19438; INCF.  
DR MGD; MGI:1314883; Tnfrsf1b.  
DR InterPro; IPR001368; TNFR\_c6.  
DR Pfam; PF00020; TNFR\_c6; 4.  
DR SMART; SM00208; TNFR; 4.  
DR PROSITE; PS00652; TNFR\_NGFR\_1; 2.

DR PROSITE; PS00650; TNFR\_NGFR\_2; 3.  
KW Receptor.  
FT NON\_TER 1 87 S -> T.  
FT VARIANT 87 93 T -> I.  
FT VARIANT 93 268 F -> I.  
FT VARIANT 268 345 S -> F.  
FT VARIANT 345 421 Y -> C.  
FT VARIANT 421 459 AA; 48686 MW; 605102; PLE46-2LDF CR664;  
SQ SEQUENCE 459 AA; 48686 MW; 605102; PLE46-2LDF CR664;

Alignment Scores:

Pred No.: 1 94e-09 Length: 459  
Score: 176.00 Matches: 50  
Percent Similarity: 43.48% Conservativity: 20  
Best Local Similarity: 31.06% Mismatches: 77  
Query Match: 18.70% Indels: 14  
DB: 11 Gaps: 8

US 09-882-735-1 (1-483) x Q62327 (1-459)

QY 10 TGTGCCCCAAGGAAAT 69  
DB 25 CysGlnIleSerGlnGluTyrTyrTyrTyrTyrTyrTyrTyrTyrTyrTyrTyrTyr 44  
QY 70 AAAGAAAT 129  
DB 45 ProGlyGlnTyrValLysHisPheCys AsnLysThrSerAspThrValCysAlaAsp 63  
QY 130 TGTGAGAGTGTCT 180  
DB 64 CysGluAlaSerMetTyrThrGlnValTyrAsnGlnIlePheArgThrCysLeuSerCysSer 83  
QY 187 TCCAAATGCCAAGGAAAT 246  
DB 84 SerSerCysSerThrAsp-----GlnValGluThrArgAlaCysThrLysGlnIleAsn 101  
QY 247 ACGT 294  
DB 102 ArgValCysAlaCysGluAlaGlyArgTyrCysAlaLeuLysThrHis SerGly 119  
QY 295 AACCTTTTCCAGTGTCT 351  
DB 120 SerCysArgGlnCysMetArgLeuSerLysCysGlyProGlyPheGlyValAlaSerSer 149  
QY 352 TGTCCAGGAAACAGAAC 438  
DB 140 ArgAlaProAsnGlyAsnValLeuCysLysAlaCysAlaProGlyThrPhe Ser 167  
QY 409 AACGAGT 468  
DB 158 AspThrThrSerSerThrAspValCysArgProHisArgIleCysSerIleLeuAlaIle 177  
QY 469 CCC 471  
DB 178 Pro 178  
RESULT 12  
Q9DGH8  
ID Q9DGH8 PRELIMINARY; PRT; 312 AA.  
AC Q9DGH8;  
DT 01-MAR-2001 (TREMURel. 16, Created)  
DT 01-MAR-2001 (TREMURel. 16, Last sequence update)  
DT 01-DEC-2001 (TREMURel. 19, Last annotation update)  
DE Fas antigen (Fragment).  
GN FAS.  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
OC Gallus.  
OX NCBI\_TaxID:9031;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Bridgham J.T., Johnson A.L.;





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DR InterPro: IPR001368; TNFR_C6.
DR Pfam: PF00020; TNFR_C6; 2
DR SMART: SM00208; TNFR; 2
DR PROSITE: PS00652; TNFR_NGFR_1
DR PROSITE: PS00652; TNFR_NGFR_2
DR PROSITE: PS00650; TNFR_NGFR_3
KW Receptor.
KW Sequence 316 AA, 34660 MW,
2
```

Alignment Scores:	
Prod. No.:	5.5e-09
Score:	171.50
Percent Similarity:	42.38%
Best Local Similarity:	27.8%
Query Match:	18.23%
DR:	12
Length:	316
Matches:	42
Conservative:	22
Mismatches:	62
Indels:	25
Gaps:	6

US 09 882-735-1 (1-483) x 057092 (1-316)

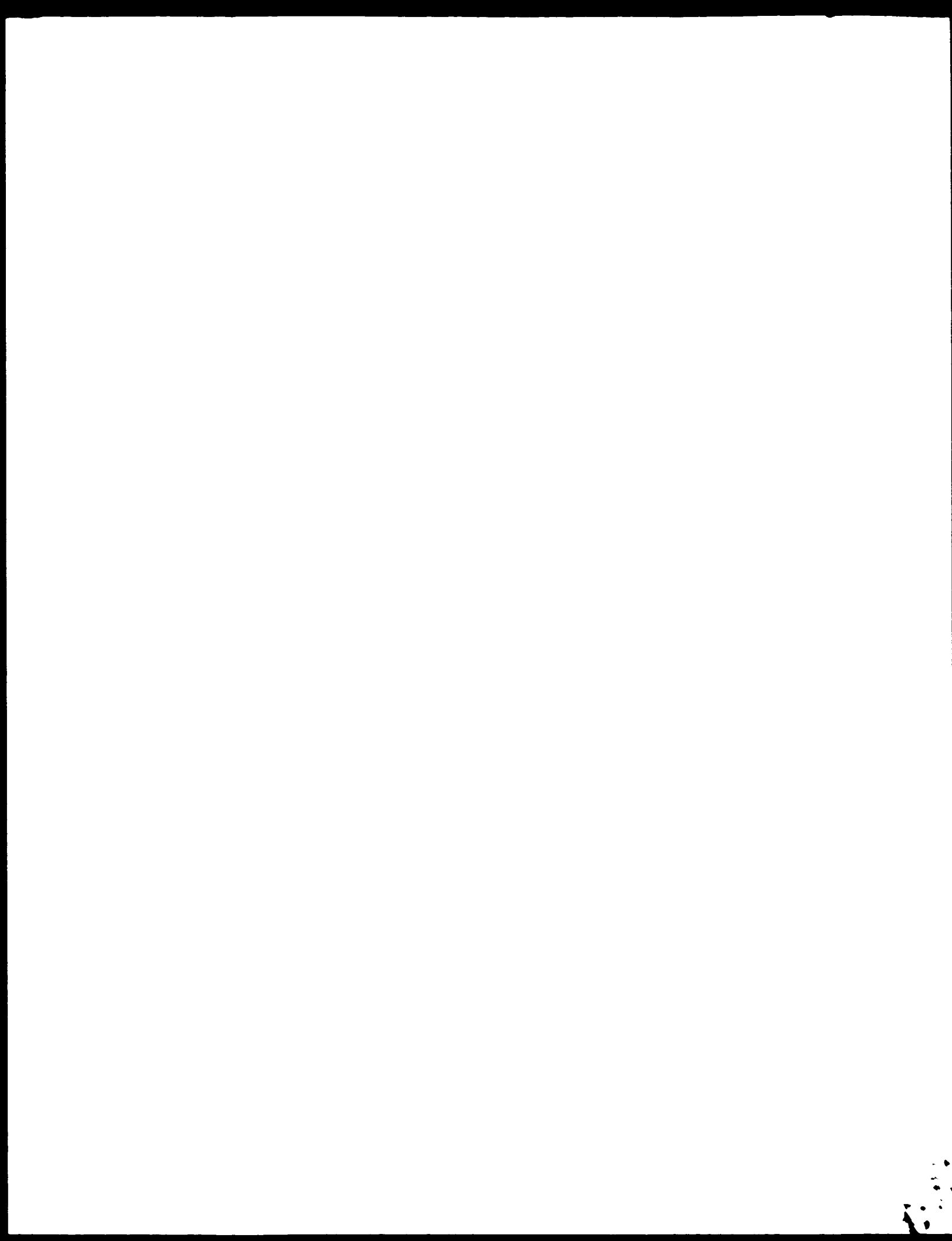
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QY 40 AATAATTCAGTTGCTGTACCACTGCCACAAAGAAACCTACTTGTACATGACTGTCTCA 996
Db 40 .....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
QY 34 SerAsnAspLeuCysCysLysGlnCysAsnProGlyMetTyrMetThrHisSerCys--- 52
Db 34 .....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
QY 106 GGCCTGGGGAGATATATATATCTCAGTGAATGTGAGAGGTCTCTTCAGAGCTTCAGAA 159
Db 106 .....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
QY 53 AsnThrThrSerAsnThrLysCysAspLysCysProAspAspThrPheThrSerIlePro 72
Db 53 .....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
QY 160 AACCACTCTACACACTGCTCTAGTTGC-----TCCAAATGCCGAAAGAAATGGGTTCAGT 216
Db 160 .....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
QY 73 AsnHisSerProAlaCysLeuSerCysArgGlyLysCys-----SerSerAsnGlnVal 90
Db 73 .....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
QY 219 GAGATCTTTCTTTCACACAGTGGACCGGGACACCGCTGTGGCTGCACAGAGAACCACTAC 276
Db 219 .....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
QY 91 GluThrLysSerCysSerAsnThrGlnAspArgValCysValCysAlaSerGlyTyrTyr 110
Db 91 .....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
QY 272 GGGCAATTATCGAATTCGAAACCTTTTCAGTCTCTTAATTGCAGCTCTGCTCAATGTT 336
Db 272 .....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
QY 111 CysGluPheGluGlySerAsn-----GlyCysArgLysCysValProGln 125
Db 111 .....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
QY 337 ACAGTGGCAATTCTATCTATCAAAACACAAACACAAAGTTCACATCGTCATCATAGTTTC 396
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QY 126 Thr-----LysCysGlySerGlyTyr 132
Db 126 .....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
QY 397 TTCTCA-----AGAGAAAAACGAGTGTGTCCTCTGTAGTAACTGAAGAAAGCGTG 447
Db 397 .....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
QY 133 GlyValTyrGlyTyrSerSerLysGlyAspValIleCysLysCysProGlyAsnIle 152
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QY 448 GAGTCGACGAGTTGTGCTTACCCACAGATTGAG 480
Db 448 .....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
QY 153 AspLysCysAspLeuSerPheAsnSerIleAsp 163
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CD	C47091;
DT	01-JUN-1998 (TrEMBLrel. 06, Created)
DT	01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT	01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE	Tumor necrosis factor receptor II homolog.
DN	CRMO.
OS	Ectromelia virus.
OC	Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
CC	Orthopoxvirus.
OX	NCBI_TaxID=12643;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=MUNICH-MP3;
FX	MEDLINE=98188282; PubMed=9520445;
RA	Loparev V.N., Parsons J.M., Knight J.C., Panus J.F., Ray C.A.,
RA	Buller R.M.L., Pickup D.J., Esposito J.J.;
RT	"A third distinct tumor necrosis factor receptor of orthopoxviruses.";
RL	Proc. Natl. Acad. Sci. U.S.A. 95:3786-3791(1998).
FR	EMBL; U87578; AAR94348.1; -;
DR	HSP; F19438; 1EXT.



QY	181	AGTGTGTTTAAATGCGAAAGAAATGGGTGAGTGGAGATCTCTTCTTGCCACAGTGGAC	240
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QY	481	AAT 483	
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DEFINITION	AR134762	Accession	
ACCESSION	AR134762	GI:14123667	
VERSION	AR134762.1	GI:14123667	
KEYWORDS	Unknown.		
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	1 (bases 1 to 1301)		
AUTHORS	Campbell, P. K., Jameson, B. A. and Chappel, S. C		
TITLE	DNA encoding a hybrid heterodimeric protein		
JOURNAL	Patent: US 6194177 A 7 27-FEB-2001;		
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[illegible]





CY 481 AAT 483  
 DB 755 AAT 757  
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 DEFINITION Human tumor necrosis factor receptor mRNA, complete cds.  
 ACCESSION M33294  
 VERSION M33294.1 GI:3339744  
 KEYWORDS cell surface receptor; tumor necrosis factor receptor.  
 SOURCE Human placenta, cDNA to mRNA.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 Schall T P, Lewis M, Koller K T, Lee A L, Rice G C, Wong G H, Gaudinaga T, Springer A, Leiber R, Radd H, Kohli M J, and Geisler T V  
 Identification, cloning and expression of a receptor for human tumor necrosis factor  
 Cell 61:1369-1376 (1990)  
 TITLE  
 JOURNAL JOURNAL OF CELLULAR PHYSIOLOGY  
 MEDLINE 90235285  
 PUBMED 2159969  
 COMMENT Direct entry and computer readable sequence for (1) kindly submitted by T.Schall, 26-MAR-1990.  
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 DB 662 AACAGAACACCGTGTGACCTGCGATGAGGTCTTTCTTTAGAGAAACAGGTGTC 721  
 CY 421 TCTGTAACTAATCTAAGAAAGCTGAAATGTAAGAAATGTTGTAAGAAATGTAAG 480  
 DB 722 TCTGTAACTAATCTAAGAAAGCTGAAATGTAAGAAATGTTGTAAGAAATGTAAG 781  
 CY 481 AAT 483  
 DB 782 AAT 784  
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 AK056611 2109 bp mRNA linear PRI 01-AUG-2002  
 LOCUS Homo sapiens cDNA FL330349 fis, clone NTNGS200120, highly similar  
 DEFINITION TO TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR  
 ACCESSION AK056611  
 VERSION AK056611.1 GI:1655062  
 KEYWORDS oligo capping; fis (full insert sequence).  
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 REFERENCE 1 Nimomiyu K, Nagatsuna M, Kanda K, Kondo H, Yokoi T, Kodaira H, Furuya T, Takahashi M, Kikawa E, Omita Y, Kishita K, Katsuta N, Sato K, Tachikawa Y, Imaizaki M, Sugiyama T, Irie R, Otsuki T, Sato H, Wakamatsu A, Ishii S, Yamamoto J, Isono Y, Kawai H, Kawai H, Saito K, Nishikawa T, Kimura K, Yamashita H, Matsuo K, Nakamura Y, Sekine M, Kikuchi H, Murakawa K, Kanehori K, Takahashi-Fujii A, Oshima A, Sugiyama A, Kawakami B, Suzuki Y, Sugano S, Nagahara K, Masuno Y, Nagai K, and Isogai T.  
 NEDO human cDNA sequencing project  
 TITLE  
 JOURNAL Nucleic Acids Res  
 MEDLINE 12111111  
 PUBMED 11511111  
 COMMENT Submitted (24-OCT-2001) Takao Isogai, Helix Research Institute, Genomics Laboratory, 153-3 Yana, Kizatsubo, Chiba 274-0812, Japan (E-mail: genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)  
 NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: RAB and HRI.  
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 DB 667 AAGAGGCAAGAGGAACTATCTGTAATATGATGTTTAAAGAGAGAGAGAGATAGGAG 726  
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 DB 727 TGAAG 786  
 QY 481 AAT 483  
 DB 787 AAT 789  
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 ACCESSION M58286 M33480  
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 1 (bases 1 to 2111)  
 Tabuchi, H., Pan, Y.C., Lahn, H.W., Gentz, R., Brockhaus, M.,  
 Molecular cloning and expression of the human 55 kd tumor necrosis  
 factor receptor  
 JOURNAL Cell 61 (2), 351-359 (1990)  
 MEDLINE 90235284  
 PUBMED 2158862  
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 QY 122 TGAAG 180  
 DB 427 TGAAG 486  
 QY 141 AAGAGGCAAGAGGAACTATCTGTAATATGATGTTTAAAGAGAGAGAGAGATAGGAG 240  
 DB 481 AAGAGGCAAGAGGAACTATCTGTAATATGATGTTTAAAGAGAGAGAGAGATAGGAG 546  
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 DB 607 GAG 666  
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 DB 667 AAGAGGCAAGAGGAACTATCTGTAATATGATGTTTAAAGAGAGAGAGAGATAGGAG 726  
 QY 421 TGAAG 480  
 DB 727 TGAAG 786  
 QY 481 AAT 483  
 DB 787 AAT 789  
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 DEFINITION M63121 M75861  
 ACCESSION M63121 M75861  
 VERSION 1.0 (1/2/93/75)  
 KEYWORDS tumor necrosis factor receptor.  
 SOURCE Human cDNA to mRNA.  
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 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo;  
 1 (bases 1 to 2112)  
 Hammer, A., Maurer-Poggy, I., Kronke, M., Scheurich, P.,  
 Pitzereimater, K., Lantzy, K., Gissen, I., Hauptmann, F., Siatkowska, C. and  
 Adolff, G.R.  
 Molecular cloning and expression of human and rat tumor necrosis  
 factor receptor chain (p60) and its soluble derivative, tumor  
 necrosis factor-binding protein  
 JOURNAL DNA Cell Biol. 9 (10), 705-715 (1990)  
 MEDLINE 91090841  
 PUBMED 1702293



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FEGLCLSLFLFGLMYPYQWKSILVCGKSTPEKEGELEGTTKPLAPNPSPT
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Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GATACGTGTGTGTCGCAAGAGAAATATATCCACCCCTCAAAATAATTCGATTTCGTGACC 60
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QY 61 AAGTGGACAAAGAACTATTGTTACAACTGTCGAGGCGCGGGGAGGATACGGAC 120
DB 387 AAGTGGACAAAGAACTATTGTTACAACTGTCGAGGCGCGGGGAGGATACGGAC 446

QY 121 TTTATGTAATCTTAAGAGATGTTCTGCTTACCGCTTCAGAAAACCACTCAGACACTGCTC 180
DB 447 TTTATGTAATCTTAAGAGATGTTCTGCTTACCGCTTCAGAAAACCACTCAGACACTGCTC 506

QY 181 AGCTCTCTCAATGCGCAAGCAAAATGGGTGAGGTGAGATCTCTCTTTCACAGTGGAC 240
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QY 241 CAGGACACGCTGTTGCTGCTTACAGAAATAATGTAATGTAATGTAATGTAATGTAATGTAAT 300
DB 567 CAGGACACGCTGTTGCTGCTTACAGAAATAATGTAATGTAATGTAATGTAATGTAATGTAAT 626

QY 301 TTCCATGTTTCAATTGAGCTTACGCTTACGCTTACGCTTACGCTTACGCTTACGCTTACGCTT 360
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QY 361 AAACAGAACAGCTGTTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTG 420
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QY 421 TCTCTATTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATG 480
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DB 807 AAT 809
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Search completed: January 6, 2003, 01:02:22  
Job time : 2791 secs



GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: January 5, 2003, 22:50:57 ; Search time 263 Seconds  
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4135.799 Million cell updates/sec

Title: US-09-882-735-1

Perfect score: 483

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Scoring table: IDENTITY NUC  
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Searched: 2185219 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DR seq length: 0

Maximum DR seq length: 200000000

Post processing: Minimum Match 0%

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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1	483	100.0	483	19	AAV41548	Human soluble tumor
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3	483	100.0	483	20	AAV81732	Tumour necrosis in
4	483	100.0	483	22	AAC83945	Human 30 kDa TNF i
5	483	100.0	1301	18	AAT54032	cDNA for TBP(20-19
6	483	100.0	1334	11	AAQ66282	Plasmid Tumour Nec
7	483	100.0	1368	21	AAQ49932	Lambda-derived TNF
8	483	100.0	1368	21	AAA95105	Human TNFp1 coding
9	483	100.0	1478	20	AAV58150	CadC-fusion polype

10	483	100.0	2062	13	AAQ20973	TNF alpha binding
11	483	100.0	2062	13	AAQ24440	Encodes TNF alpha
12	483	100.0	2088	12	AAQ10883	30kD TNF inhibitor
13	483	100.0	2088	22	AAC83946	Human 30 kDa TNF i
14	483	100.0	2111	12	AAQ10955	Encodes human 30kD
15	483	100.0	2111	20	AAZ09170	Human tumour necro
16	483	100.0	2111	22	AAH48859	Human TNFRp1 associ
17	483	100.0	2111	22	AAH48859	Human TNFRp1 associ
18	483	100.0	2111	24	ABP84039	Human cDNA differe
19	483	100.0	2161	21	ABP9582	Gene #246 used to
20	483	100.0	2161	21	AZ48475	Human tumour necro
21	483	100.0	2161	24	ABK13194	Human tumour necro
22	483	100.0	2175	16	AAQ90513	p55 TNF Receptor
23	483	100.0	6889	17	AAT15931	DiPP/Inten (WTAS)
24	483	100.0	6926	18	AAV04431	Vector pCDNA3.1(+)
25	483	100.0	2141	11	AAQ06285	Human Tumour Necro
26	483	100.0	2176	12	AAQ12315	Type 1 TNF receptor
27	483	100.0	2170	14	AAQ50870	Human Tumour Necro
28	483	100.0	608	13	AAQ24441	Encodes truncated
29	483	100.0	1147	18	AAT94021	cDNA for TBP(20-19
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31	483	100.0	1202	18	AAT94008	cDNA for TBP(20-19
32	483	100.0	1674	21	AAZ50196	Male fusion plasmid
33	483	100.0	504	13	AAQ24445	Encodes truncated
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36	483	100.0	339	19	AAV19804	Truncated stnfr, s
37	483	100.0	333	19	AAV19805	Truncated stnfr, s
38	483	100.0	332	19	AAV19803	Truncated stnfr, s
39	483	100.0	2130	24	ABP63694	Rat sequence diffe
40	483	100.0	5870	21	AAV15044	Nucleotide sequen
41	483	100.0	315	11	AAQ66294	Rat Tumour Necro
42	483	100.0	315	19	AAV19806	Truncated stnfr, s
43	483	100.0	294	19	AAV19808	Truncated stnfr, s
44	483	100.0	285	19	AAV19807	Truncated stnfr, s
45	483	100.0	1497	21	AAZ50194	Male fusion plasmid

#### ALIGNMENTS

RESULT 1  
AAV41548  
ID AAV41548 standard; cDNA; 483 BP.  
AC AAV41548;  
XX  
DT 28-SEP-1998 (first entry)  
XX  
DE Human soluble tumour necrosis factor receptor type 1.  
XX  
KW Human; tumour necrosis factor, TNF; TNF receptor type 1;  
KW inflammatory disease; leukaemia; TNF binding protein;  
KW anti-inflammatory drug; methotrexates; ss.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
CDS 1..483  
FT /\*tag= a  
FT /product= "human soluble TNF receptor type 1"  
XX  
PN WQ9824463-A2.  
XX  
PD 11-JUN-1998.  
XX  
PF 08-DEC-1997; 97WO-US22733.  
XX  
PE 09-JUL-1997; 97US-0052023.  
PE 06-DEC-1996; 96US-0032587.  
PE 23-JAN-1997; 97US-0036355.  
PE 07-FEB-1997; 97US-0039315.  
XX













XX (GENA) GENAISSANCE PHARM INC.  
 PA (NAND/) NANDARALAN K.  
 PA (SCHU/) SCHULZ V P.  
 PA (STEP/) STEPHENS J C.  
 PA (CHEW/) CHEW A.  
 XX  
 PI Nandabalan K, Schulz VP, Stephens JC, Chew A;  
 XX  
 XX WPI; 2000-543909/49.  
 DR P-PSDB; AAR21446.  
 XX  
 XX Polynucleotides comprising polymorphic variants of a reference sequence  
 PT for tumour necrosis factor receptor 1 (TNFR1), useful for studying the  
 PT biological function of TNFR1 and identifying drugs targeting the  
 PT protein for treating disorders.  
 XX  
 PS "Claim 7; Fig 4; 79pp; English.  
 XX  
 CC The present invention relates to polymorphic variants of the tumour  
 CC necrosis factor receptor 1 (TNFR1) gene. The present sequence is  
 CC the coding sequence of the TNFR1 gene. The sequence of the whole gene is  
 CC given in AAA95102, AAA95103 and AAA95104. The polymorphisms were  
 CC identified by amplifying and sequencing regions of the gene. Twelve  
 CC polymorphic loci were discovered. Of these twelve polymorphisms, four can  
 CC cause a change in the TNFR1 protein. The TNFR1 polymorphisms may be  
 CC useful for studying the biological function of TNFR1 as well as for  
 CC identifying drugs targeting the protein for treatment of disorders  
 CC related to its abnormal expression or function such as tumours,  
 CC apoptosis related disorders and bacterial infection.  
 XX  
 SQ Sequence 1368 BP; 202 A; 424 C; 376 G; 276 T; 0 other;  
 Query Match 100.0%; Score 483; DB 21; Length 1368;  
 Best Local Similarity 100.0%; Pred No. 1.5e-140;  
 Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

QY 1 GATATGTGTGTGTCGCAAGGAAATATATATACACCTTAAATATATGATTTGTGTACC 60  
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 DB |||||  
 QY 181 AAGTGTGTGTGTCGCAAGGAAATATATATACACCTTAAATATATGATTTGTGTACC 240  
 DB |||||  
 QY 121 TGACGAGAGTGTGTGACAGGAGGTCCTTCCACCTTACAGAAACCCACCTCAGACACTGCCTC 180  
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 QY 241 TGACGAGAGTGTGTGACAGGAGGTCCTTCCACCTTACAGAAACCCACCTCAGACACTGCCTC 300  
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 DB |||||  
 QY 361 GCGACACCTGTGTGTGTCGCAAGGAAATATATATACACCTTAAATATATGATTTGTGTACC 420  
 DB |||||  
 QY 301 TTTCAGTGTGTGTGTCGCAAGGAAATATATATACACCTTAAATATATGATTTGTGTACC 360  
 DB |||||  
 QY 421 TTTCAGTGTGTGTGTCGCAAGGAAATATATATACACCTTAAATATATGATTTGTGTACC 480  
 DB |||||  
 QY 361 AAACAGACACCTGTGTGTCGCAAGGAAATATATATACACCTTAAATATATGATTTGTGTACC 420  
 DB |||||  
 QY 481 AAACAGACACCTGTGTGTCGCAAGGAAATATATATACACCTTAAATATATGATTTGTGTACC 540  
 DB |||||  
 QY 421 TTCTGTAGTGTGTGTCGCAAGGAAATATATATACACCTTAAATATATGATTTGTGTACC 480  
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 QY 541 TTCTGTAGTGTGTGTCGCAAGGAAATATATATACACCTTAAATATATGATTTGTGTACC 600  
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 QY 481 AAT 483  
 DB |||||  
 QY 601 AAT 603

RESULT 9  
 AAX58150  
 ID AAX58150 standard; DNA; 1478 BP.  
 XX  
 AC AAX58150;  
 XX  
 DT 21-JUL-1999 (first entry)  
 XX  
 DE CadC-fusion polypeptide coding sequence.  
 XX  
 KW CadC; fusion protein; tumour necrosis factor alpha interaction domain;  
 KW protein-protein interaction; periplasmic domain; transmembrane domain;  
 KW CadC transcriptional regulatory domain; receptor interaction;  
 KW ligand identification; orphan receptor; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9923116-A1.  
 XX  
 PD 14-MAY-1999.  
 XX  
 PF 03-NOV-1998; 98WO-US23307.  
 XX  
 PR 09-SEP-1998; 98US-0149922.  
 PR 03-NOV-1997; 97US-0064058.  
 XX  
 PA (SMAL-) SMALL MOLECULE THERAPEUTICS INC.  
 XX  
 PI Hsing W, Menzel R, Taggart PA;  
 XX  
 DR WPI; 1999-313305/26.  
 XX  
 PT New CadC-fusion polypeptide nucleic acid constructs  
 XX  
 PS Claim 4, Fig 3a, 123pp, English.  
 XX  
 CC This sequence encodes a CadC-fusion polypeptide containing the  
 CC tumour necrosis factor alpha interaction domain.  
 CC The invention relates to CadC-fusion polypeptide nucleic acid constructs,  
 CC which are used to transform cells to produce systems for identifying  
 CC compounds which modulate interactions between protein sequences. The  
 CC CadC-fusion polypeptides comprise a periplasmic domain, a transmembrane  
 CC domain and a CadC transcriptional regulatory domain. Cells transformed  
 CC with nucleic acid encoding the fusion proteins and a cadA reporter  
 CC construct can be used for identifying compounds which modulate a specific  
 CC protein-protein interaction such as modulation of interactions between  
 CC protein sequences involved in receptor interactions, e.g. dimerisation.  
 CC Such methods can be used for identifying ligands for orphan receptors.  
 CC The system is extremely sensitive in that background is low and the  
 CC magnitude of signal background is quite robust, such that even minor  
 CC modulations in protein-protein interactions are readily detectable.  
 XX  
 SQ Sequence 1478 BP; 398 A; 351 C; 346 G; 381 T; 2 other;  
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 Best Local Similarity 100.0%; Pred. No. 1.5e-140;  
 Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

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[illegible][illegible]

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 FT 274..1551 /\*tag= b  
 FT /product= 55kd TNF-BP  
 XX  
 PN EP417563 A.  
 XX  
 PD 20 MAR 1991.  
 XX  
 PF 31 AUG 1990; 90EP-0116707.  
 XX  
 PR 20 APR 1990; 90CH-0001347.  
 PR 12 SEP 1989; 89CH-0003319.  
 XX 08 MAR 1990; 90CH-0000746.  
 XX (HOFF ) HOFFMANN-LA ROCHE AG.  
 PA  
 XX Brockhaus M, Dembic Z, Gentz R, Lesslauer W, Lotscher H;  
 PI Schlaefer E;  
 XX  
 DR WPI, 1991-081951/12.  
 DR F PSDB; AAR11082.  
 XX  
 PT Insoluble tumour necrosis factor binding proteins - and DNA  
 PT encoding them, useful in pharmaceutical prods. and for antibody  
 PT prodn.  
 XX  
 PS Claim 4; Fig 1; 26pp; German.  
 XX  
 CC Partial amino acid sequences were determined for the 55 and 75kd  
 CC TNF-BPs (see AAP11072-B11081) and oligonucleotide primers were  
 CC synthesised based on these partial sequences. The primers were used  
 CC to produce a cDNA fragment for use as a probe to screen a human  
 CC placental cDNA bank constructed in lambda gt11. Positive clones were  
 CC identified and sequenced. DNA constructs comprising the TNF-BP coding  
 CC sequence may also contain a fragment encoding a human Ig domain.  
 CC Recombinant constructs are used to transform cells to confer  
 CC improved TNF-binding properties.  
 CC See also AAQ10956.  
 XX  
 SQ Sequence 2111 BP; 445 A; 628 C; 588 G; 450 T; 0 other;

Query Match 100.0%; Score 483; DR 12; Length 2111;  
 Best Local Similarity 100.0%; Pred No 1 Re-140;  
 Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0.  
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 QY 61 AAGTCCGACAAAGAACTTCTTTTACAAATGACTGTCGAGCGCGCGGAGATACGGAC 120  
 DB |||||||  
 QY 162 AAGTCCGACAAAGAACTTCTTTTACAAATGACTGTCGAGCGCGCGGAGATACGGAC 426  
 DB |||||||  
 QY 121 TGCAGGAGTTGTCAGAGCGGCTTCTTACCGCTTACAGAAACACCTCAGACACTGGCTC 180  
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 QY 427 TCGAGGATTTGAGAAATGAGTCTTCTTACAGAAACACCTCAGACACTGGCTC 486  
 DB |||||||  
 QY 181 AGCTCTCTCAAAATGCGGAGAAATGAGTCTTCTTACAGAGATCTCTTCTTCCAGCTGGAC 240  
 DB 487 AGCTCTCTCAAAATGCGGAGAAATGAGTCTTCTTACAGAGATCTCTTCTTCCAGCTGGAC 546  
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 DB 607 TTTGAGTGTCTTAAATTAAGCTTCTTCTTCAATGGGACCGGCTCTCTCTCCAGGAG 666  
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 DB 667 AAACAGACAGGATTTCTTCTTACAGAACTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 726

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 DB 787 AAT 789  
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 AC AAZ09170;  
 XX  
 DT 18-OCT-1999 (first entry)  
 XX  
 DE Human tumour necrosis factor binding protein cDNA.  
 XX  
 KW Tumour necrosis factor binding protein; TNF; insoluble protein; agonist;  
 KW anti-inflammatory; antimalarial; treatment; septic shock; inflammation;  
 KW autoimmune glomerulonephritis; cerebral malaria; immune response;  
 KW antagonist; diagnosis; ds.  
 XX  
 OS Homo sapiens.  
 XX  
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 FT CDS 187..1554  
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 FT /product= "TNF binding protein"  
 FT sig\_peptide 187..273  
 FT /\*tag= b  
 FT mat\_peptide 274..1551  
 FT /\*tag= c  
 XX  
 PN EP939121-A2.  
 XX  
 PD 01-SEP-1999.  
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 PF 31-AUG-1990, 90EP-0116707  
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 PR 20-APR-1990, 90CH-0001347.  
 PR 12-SEP-1989; 89CH-0003319.  
 PR 08-MAR-1990, 90CH-0000746.  
 XX  
 XX (HOFF ) HOFFMANN-LA ROCHE & CO AG F.  
 XX  
 PI Brockhaus M, Dembic Z, Gentz R, Lesslauer W, Lotscher H;  
 PI Schlaefer E;  
 XX  
 DP WPI; 1990-480840/41  
 DR P-PSDB; AAY30934.  
 XX  
 PT New insoluble proteins, and fragments, that bind to tumor necrosis  
 PT factor, used to treat e.g. septic shock or cerebral malaria  
 XX  
 PS Claim 4; Fig 1; 25pp; German.  
 XX  
 CC This invention describes novel homogeneous insoluble proteins (I),  
 CC their (insoluble) fragments (Ia) and their salts that can bind tumour  
 CC necrosis factor (TNF). The products of the invention have  
 CC anti-inflammatory and antimalarial activity. (I) and (Ia) are used (i)  
 CC to treat diseases in which TNF is involved (e.g. septic shock, autoimmune  
 CC glomerulonephritis, cerebral malaria, immune responses and inflammation).  
 CC (ii) to purify TNF. (iii) to identify TNF (antagonists and (iv) for  
 CC diagnostic determination of TNF in body fluids. Antibodies raised against  
 CC (I) are used for affinity purification of (I). This sequence encodes  
 CC a tumour necrosis factor binding protein described in the method of  
 CC the invention.  
 XX  
 SQ Sequence 2111 BP; 445 A; 629 C; 587 G; 450 T; 0 other;



GenCore version 5.1.3  
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OM nucleic nucleic search, using sw model

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Title: US-09-882-735-1

Perfect score: 483

Sequence: 1 dataatgtgtgtcccaagg gctaccacagattgagaat 483

Scoring table: IDENTITY NUC

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Searched: 441362 seqs, 15338381 residues

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Minimum DB seq length: 0

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Maximum Match 100%

Listing first 45 summaries

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- 5: /cgn2\_6/ptodata/1/ina/pCTUS\_COMB seq.\*
- 6: /cgn2\_6/ptodata/1/ina/backfile1 seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	483	100.0	1301	4	US-08-804-166-7
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4	483	100.0	1478	4	US-09-149-922-6
5	483	100.0	2062	1	US-08-050-319B-24
6	483	100.0	2062	2	US-08-465-982-49
7	483	100.0	2161	3	US-09-106-038A-1
8	483	100.0	2161	4	US-09-505-250-3
9	483	100.0	2175	1	US-08-321-668-1
10	483	100.0	2175	1	US-08-837-941-1
11	483	100.0	2175	1	US-08-126-016-1
12	483	100.0	2175	4	US-08-054-970-1
13	483	100.0	6889	1	US-08-286-740-2
14	483	100.0	6889	5	PCT-US95-09576-2
15	483	100.0	6889	2	US-08-627-151A-6
16	475.2	98.4	600	2	US-08-050-319B-47
17	475.2	98.4	600	2	US-08-465-982-47
18	475	98.3	1147	4	US-08-804-166-5
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20	424.4	87.9	1049	4	US-08-804-166-1
21	424.4	87.9	1049	4	US-08-910-991-1
22	424.4	87.9	1202	4	US-08-804-166-3
23	424.4	87.9	1202	4	US-08-910-991-3
24	383	79.3	504	1	US-08-050-319B-56
25	383	79.3	504	2	US-08-465-982-56
26	381	78.9	501	1	US-08-050-319B-1
27	381	78.9	501	2	US-08-465-982-1

Sequence 1, Appl:  
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Sequence 49, Appl:  
Sequence 49, Appl:  
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ALIGNMENTS

RESULT 1  
US-09-326-394-1  
; Sequence 1, Application US/09326394  
; Patent No. 6306820  
; GENERAL INFORMATION:  
; APPLICANT: Bendele, Alison M.  
; APPLICANT: Sennello, Regina M.  
; APPLICANT: Edwards, Carl K.  
; TITLE OF INVENTION: COMBINATION THERAPY USING A TRP BINDING  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Amgen Inc.  
; STREET: 1840 DeHavilland Drive  
; CITY: Thousand Oaks  
; STATE: CA  
; COUNTRY: US  
; ZIP: 91320-1789  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1 0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/326,394  
; FILING DATE: 08-DEC-1997  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/032,587  
; FILING DATE: 06-DEC-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/036,355  
; FILING DATE: 23-JAN-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/039,315  
; FILING DATE: 07-FEB-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/052,023  
; FILING DATE: 09-JUL-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Zindrick, Thomas K.  
; REGISTRATION NUMBER: 32,185  
; REFERENCE/DOCKET NUMBER: A-430D  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 483 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: unknown  
; TOPOLOGY: unknown  
; MOLECULE TYPE: CDNA

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;      FEATURE:
;      NAME/KEY: CDS
;      LOCATION: 1..483
US-09-326-394-1

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Query Match	100.0%	Score 483;	DB 4;	Length 483;
Best Local Similarity	100.0%	Pred. No. 2.8e-146;		
Matches 483;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

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Db  
241 CCGAAACGCTGTGGCTGACGAGAGAACCTACCGGCAATTATTGGAGTGAACCTT 300  
501 TTTCAGTGGTCAATTCACCGTCGCTCAATGCGACCGTCGCGACGAG 360

Dp 301 ATTACGATTATTCAGCAAGCTCTGCTCATATGACAGCTGACCTCTCTGACAGAG 360  
 Oy 361 AAACAAATAATGCTGTGATCTGTGATGACAGATTCTTTCTTAGCAAAAACGATGTGTC 420

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421  TCTCTGATGTAATTGTAAAGGAGCTGAGTGCACAGAGTTGGCTACCCAGATTGAG 480
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Qy	481	AAT	483
Db	481	AAT	483

RESULT 2  
US-08-004-16-7  
Case:080007 Petitioner:mc/0800166

Sequence / Application US/0004166  
Patent No. 6193972  
GENERAL INFORMATION:  
APPLICANT: Campbell, Robert K.  
APPLICANT: Jameson, Bradford A.

APPLICANT: Chapel, Scott C.  
TITLE OF INVENTION: HYPERID PROTEINS  
NUMBER OF SEQUENCES: 22  
CORRESPONDENCE ADDRESS:

ADDRESS: BROWDY AND BELMARR  
STREET: 419 Seventh Street N.W., Ste. 300  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA

ZIP: 22207  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible

```

1 OPERATING SYSTEM: PC-DOS/MS-POS
2 SOFTWARE: ParentIn Release #1.0, Version #1.30
3 CURRENT APPLICATION DATA:
4 APPLICATION NUMBER: US/08/834,166
5 FILING DATE:

```

FILE NO. 100-441101  
CLASSIFICATION: UNCLASSIFIED  
PRIOR APPLICATION DATA: 100-441101

```

1  APPLICATION NUMBER: 60/011,936
2  FILING DATE: 20 February 1996
3  CLASSIFICATION:
4  ATTORNEY/AGENT INFORMATION:
5  NAME: Browdy, Roger L.
6  REGISTRATION NUMBER: 25,618
7  REFERENCE/DOCKET NUMBER: CAMPELL=2A
8  TELECOMMUNICATION INFORMATION:
9  TELEPHONE: (202) 628-5197
10  TELEFAX: (202) 737-3528
11  INFORMATION FOR SEQ ID NO.: 7:
12  SEQUENCE CHARACTERISTICS:
13  LENGTH: 1301 base pairs
14  TYPE: nucleic acid
15  STRANDEDNESS: single
16  TOPOLOGY: linear
17  MOLECULE TYPE: cDNA
18  FEATURE:
19  NAME/KEY: CDS
20  LOCATION: 279..1287
21  US-08-804-166-7

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Query Match	100.0%;	Score 483;	DB 4;	Length 1301;
Best Local Similarity	100.0%;	Pred. No. 4.5e-146;		
Matches 483;	Conservative	0;	Mismatches	0;
			Indels	0;
			Gaps	0;

Oy 1 GATGGTGTGTGCCCCAGGAAATATATTCACCCCTAAATATTCGATTGCTGTACC 60  
 Db 345 GATGGTGTGTGCCCCAGGAAATATATTCACCCCTAAATATTCGATTGCTGTACC 404

0y AAAGCCACAAAGAACTCTACTGTACAAATACATGTCACAGCCCCGAGGATACGAC 120  
 61 AAAGCCACAAAGAACTCTACTGTACAAATACATGTCACAGCCCCGAGGATACGAC 120  
 Db AAAGCCACAAAGAACTCTACTGTACAAATACATGTCACAGCCCCGAGGATACGAC 464  
 405 AAAGCCACAAAGAACTCTACTGTACAAATACATGTCACAGCCCCGAGGATACGAC 464  
 121 TGACGGAAGTGTAGAAGCGCTCTCTCAACGCTCAGAAACCACTCAGACATGCTCC 180

Db 465 TGCAGGAGATGTAGAGCGGCTCCTTCACCGCTTCAGAAAACCACTCAGACACTGGCTC 524

Db	525	AGCTGCTCCAAATGCGGAAGAAATGGGTCAGGTGGAGATCTTCTTGCAACAGTGGAC	584
Qy	241	CGGGAACCGTGTGTGGCTGCAGGAAGAACCACTACCGGATTTATTTGGAGTAAACCTT	300

[illegible]

695 ATTAGGCTCAATTGGACGCTTGGCTCAATTGGACGCTTGGCTTGGACGAG 704  
 705 AACGAGAACCGGTGACCTGCGCATGACGGTTCTTTTAAGAGAAACGAGTGTG 764  
 361 AAACGAGAACCGGTGTCATCTGCAATGACGATTTCTTTTAAGAGAAACGAGTGTG 420

OY 421 TCGTGTAGTAGTCTGTAAGAAAACCTGGAGTGCACGAATGTGTCCCTACCACGATTGAG 480  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Le 765 TCCTGTAGTAGTACTGTAGAAGAAAGCCTGTGAGTGCAAGAAATGTGTCCCTACCACGATTGAG 824

QY	481	AAT	483
Db	825	AAT	827

RESULT 3  
US-08-910-991-7  
; Sequence 7, Application US/08910991

; Patent No. 6194177  
;  
; GENERAL INFORMATION:  
;  
; APPLICANT: Campbell, Robert K.  
; APPLICANT: Jameson, Bradford A.  
; APPLICANT: Jameson, Bradford A.  
; APPLICANT: Jameson, Bradford A.

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CORRESPONDENCE ADDRESS:  
 ADDRESSEE: BROWDY AND NEIMARK  
 STREET: 419 Seventh Street N.W., Ste. 300  
 CITY: Washington  
 STATE: D.C.  
 COUNTRY: USA  
 ZIP: 22207  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/910,991  
 FILING DATE:  
 CLASSIFICATION: 530  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/004,166  
 FILING DATE: 20 February 1997  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 60/011,936  
 FILING DATE: 20 February 1996  
 ATTORNEY/AGENT INFORMATION:  
 NAME: YUN, Allen C.  
 REGISTRATION NUMBER: 37,971  
 REFERENCE/DOCKET NUMBER: CAMPBELL-28  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (202) 628-5197  
 TELEFAX: (202) 737 3528  
 INFORMATION FOR SEQ ID NO: 7:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1301 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 279..1287  
 US 08 910-991.7

Query Match 100.0%; Score 483; DB 4; Length 1301;  
 Best Local Similarity 100.0%; Pred No. 4.5e-146;  
 Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GATAGTGTGTGTCGCCCAAGGAAATATATCCACCCCTCAAAAATAATTCGATTTCGTGACC 60  
 DB 345 GATAGTGTGTGTCGCCCAAGGAAATATATCCACCCCTCAAAAATAATTCGATTTCGTGACC 404  
 QY 61 AAGTGCACAAAGGAACCTTCTGTACAAATGACTGTCCAGGCCCGGGGCGAGGATACGGAC 120  
 DB 405 AAGTGCACAAAGGAACCTTCTGTACAAATGACTGTCCAGGCCCGGGGCGAGGATACGGAC 464  
 QY 121 TGCAGGAGTGTGAGAGCGGTCTCTTCCAGCCCTTCAGAAAACCACTCAGACACTGCCTC 180  
 DB 465 TGCAGGAGTGTGAGAGCGGTCTCTTCCAGCCCTTCAGAAAACCACTCAGACACTGCCTC 524  
 QY 181 AGTGTCTCAAAATGCGAAAGAAATG99TTCAGGTGAGATCTCTCTTCGACAGTGGAC 240  
 DB 525 AGTGTCTCAAAATGCGAAAGAAATG99TTCAGGTGAGATCTCTCTTCGACAGTGGAC 584  
 QY 241 CGGACACCGTGTGTGTCGAGGAGAAACAGTACCGGCATTATTCGAGTGAACCTT 300  
 DB 585 CGGACACCGTGTGTGTCGAGGAGAAACAGTACCGGCATTATTCGAGTGAACCTT 644  
 QY 301 TTCCAGTGTCTCAATTCGAGTGTGTGTCGAGGAGAAACAGTACCGGCATTATTCGAGTGAACCTT 360  
 DB 645 TTCCAGTGTCTCAATTCGAGTGTGTGTCGAGGAGAAACAGTACCGGCATTATTCGAGTGAACCTT 704  
 QY 361 AAACAGAACACCGTGTGTGTCGAGGAGAAACAGTACCGGCATTATTCGAGTGAACCTT 420  
 DB 705 AAACAGAACACCGTGTGTGTCGAGGAGAAACAGTACCGGCATTATTCGAGTGAACCTT 764

QY 421 TCCTGTAGTAACTGTAGCAAAAGGCTTGGATGTGACGAAAGTGTGCTATGTCGACATTGAG 480  
 DB 765 TCCTGTAGTAACTGTAGCAAAAGGCTTGGATGTGACGAAAGTGTGCTATGTCGACATTGAG 824  
 QY 481 AAT 483  
 DB 825 AAT 827  
 RESULT 4  
 US-09-149-922-6  
 ; Sequence 6, Application US/09:49922A  
 ; Patent No. 6265174  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Menzel, Rolf  
 ; APPLICANT: Hsing, Weihong  
 ; APPLICANT: Taggart, Pamela  
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR IDENTIFYING AND MODULATING  
 ; TITLE OF INVENTION: PROTEIN-PROTEIN INTERACTIONS  
 ; FILE REFERENCE: 9366-006  
 ; CURRENT APPLICATION NUMBER: US/09/149,922A  
 ; CURRENT FILING DATE: 1998-09-09  
 ; EARLIER APPLICATION NUMBER: 60/064,058  
 ; EARLIER FILING DATE: 1997-11-03  
 ; NUMBER OF SEQ ID NOS: 57  
 ; SOFTWARE: Patent In Ver. 2.0  
 ; SEQ ID NO 6  
 ; LENGTH: 1478  
 ; TYPE: DNA  
 ; ORGANISM: Escherichia coli  
 ; FEATURE:  
 ; NAME/KEY: modified\_base  
 ; LOCATION: 58  
 ; OTHER INFORMATION: n-a, c, g, or t  
 ; FEATURE:  
 ; NAME/KEY: modified\_base  
 ; LOCATION: 105  
 ; OTHER INFORMATION: n-a, c, g, or t  
 US-09-149-922-6

Query Match 100.0%; Score 483; DB 4; Length 1478;  
 Best Local Similarity 100.0%; Pred No. 4.8e-146;  
 Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GATAGTGTGTGTCGCCCAAGGAAATATATCCACCCCTCAAAAATAATTCGATTTCGTGACC 60  
 DB 941 GATAGTGTGTGTCGCCCAAGGAAATATATCCACCCCTCAAAAATAATTCGATTTCGTGACC 1000  
 QY 61 AAGTGCACAAAGGAACCTTCTGTACAAATGACTGTCCAGGCCCGGGGCGAGGATACGGAC 120  
 DB 1001 AAGTGCACAAAGGAACCTTCTGTACAAATGACTGTCCAGGCCCGGGGCGAGGATACGGAC 1060  
 QY 121 TGCAGGAGTGTGAGAGCGGTCTCTTCCAGCCCTTCAGAAAACCACTCAGACACTGCCTC 180  
 DB 1061 TGCAGGAGTGTGAGAGCGGTCTCTTCCAGCCCTTCAGAAAACCACTCAGACACTGCCTC 1120  
 QY 181 AGTGTCTCAAAATGCGAAAGAAATG99TTCAGGTGAGATCTCTCTTCGACAGTGGAC 240  
 DB 1121 AGTGTCTCAAAATGCGAAAGAAATG99TTCAGGTGAGATCTCTCTTCGACAGTGGAC 1180  
 QY 241 CGGACACCGTGTGTGTCGAGGAGAAACAGTACCGGCATTATTCGAGTGAACCTT 300  
 DB 1181 CGGACACCGTGTGTGTCGAGGAGAAACAGTACCGGCATTATTCGAGTGAACCTT 1240  
 QY 301 TTCCAGTGTCTCAATTCGAGTGTGTGTCGAGGAGAAACAGTACCGGCATTATTCGAGTGAACCTT 360  
 DB 1241 TTCCAGTGTCTCAATTCGAGTGTGTGTCGAGGAGAAACAGTACCGGCATTATTCGAGTGAACCTT 1300  
 QY 361 AAACAGAACACCGTGTGTGTCGAGGAGAAACAGTACCGGCATTATTCGAGTGAACCTT 420  
 DB 1301 AAACAGAACACCGTGTGTGTCGAGGAGAAACAGTACCGGCATTATTCGAGTGAACCTT 1460  
 QY 421 TCCTGTAGTAACTGTAGCAAAAGGCTTGGATGTGACGAAAGTGTGCTATGTCGACATTGAG 480

Db 1361 TCCGTAGTAACTGTAAGAAAATCTGTGAGTGCAGAACTTGCCCTACCCGAGATTGAG 1420  
QY 481 AAT 483  
Db 1421 AAT 1423

## RESULT 5

US-08-050-319B-24  
Sequence 24, Application US/08050319B  
Patent No. 5633145  
GENERAL INFORMATION:  
APPLICANT: M. Feldmann, P.W. Gray,  
APPLICANT: M.J.C. Turner, F.M. Brennan  
TITLE OF INVENTION: Modified human TNFalpha (Tumor  
Necrosis Factor alpha) Receptor  
NUMBER OF SEQUENCES: 57  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Reed & Robbins  
STREET: 635 Bryant Street  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94301  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/050,319B  
FILING DATE: 10-May-1993  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Robbins, Roberta L.  
REGISTRATION NUMBER: 33,208  
REFERENCE/DOCKET NUMBER: 5150-0030  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 617-8999  
TELEFAX: (415) 327-3231  
INFORMATION FOR SEQ ID NO: 24  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2062 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA to mRNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 155..1519  
US-08-050-319B-24

Query Match 100.0%; Score 483; DB 1; Length 2062;  
Best Local Similarity 100.0%; Pred. No. 5,7e-146;  
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GATAGTGTGTGTGTCGTCGAGAGAAACCAATGATATATGATTTGATTGCTGATCC 60  
DB 275 GATAGTGTGTGTGTCGTCGAGAGAAACCAATGATATATGATTTGATTGCTGATCC 334  
QY 61 AAGTGTGTGTGTCGTCGAGAGAAACCAATGATATATGATTTGATTGCTGATCC 120  
DB 335 AAGTGTGTGTGTCGTCGAGAGAAACCAATGATATATGATTTGATTGCTGATCC 394  
QY 121 TCCGTAGTAACTGTAAGAAAATCTGTGAGTGCAGAACTTGCCCTACCCGAGATTGAG 180  
DB 1421 TCCGTAGTAACTGTAAGAAAATCTGTGAGTGCAGAACTTGCCCTACCCGAGATTGAG 454  
QY 151 AAT 483  
DB 481 AAT 483  
QY 481 AAT 483  
DB 481 AAT 483

QY 241 CGGACACCGTGTGTGTCGTCGAGAGAAACCAATGATATATGATTTGATTGCTGATCC 300  
DB 515 CGGACACCGTGTGTGTCGTCGAGAGAAACCAATGATATATGATTTGATTGCTGATCC 574  
QY 301 TTCGATGTAACTGTAAGAAAATCTGTGAGTGCAGAACTTGCCCTACCCGAGATTGAG 360  
DB 575 TTCGATGTAACTGTAAGAAAATCTGTGAGTGCAGAACTTGCCCTACCCGAGATTGAG 634  
QY 361 AACGAGAACCGTGTGTGTCGTCGAGAGAAACCAATGATATATGATTTGATTGCTGATCC 420  
DB 635 AACGAGAACCGTGTGTGTCGTCGAGAGAAACCAATGATATATGATTTGATTGCTGATCC 694  
QY 421 TCCGTAGTAACTGTAAGAAAATCTGTGAGTGCAGAACTTGCCCTACCCGAGATTGAG 480  
DB 695 TCCGTAGTAACTGTAAGAAAATCTGTGAGTGCAGAACTTGCCCTACCCGAGATTGAG 754  
QY 481 AAT 483  
DB 755 AAT 757

## RESULT 6

US-08-465-982-24  
Sequence 24, Application US/08465982  
Patent No. 5633786  
GENERAL INFORMATION:  
APPLICANT: M. Feldmann, P.W. Gray,  
APPLICANT: M.J.C. Turner, F.M. Brennan  
TITLE OF INVENTION: Modified human TNFalpha (Tumor  
Necrosis Factor alpha) Receptor  
NUMBER OF SEQUENCES: 57  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Reed & Robbins  
STREET: 635 Bryant Street  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94301  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/465,982  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/050,319  
FILING DATE: 10-May-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Robbins, Roberta L.  
REGISTRATION NUMBER: 33,208  
REFERENCE/DOCKET NUMBER: 5150-0030  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 617-8999  
TELEFAX: (415) 327-3231  
INFORMATION FOR SEQ ID NO: 24  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2062 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA to mRNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 155..1519  
US-08-465-982-24

Query Match 100.0%; Score 483; DB 2; Length 2062;  
Best Local Similarity 100.0%; Pred. No. 5,7e-146;  
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;











NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESS: Gen-Probe Incorporated  
STREET: 10210 Genetic Center Drive  
CITY: San Diego  
STATE: CA  
COUNTRY: USA  
ZIP: 92121  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/627,151A  
FILING DATE: 03-APR-1996  
CLASSIFICATION: 435  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Fisher, Carlos A.  
REGISTRATION NUMBER: 36,510  
REFERENCE/DOCKET NUMBER: CB1016  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-410-8926  
TELEFAX: 619-410-8928  
TELEX:  
INFORMATION FOR SEQ ID NO: 6.  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6896 base pairs  
TYPE: nucleic acid  
STRADEDNESS: single  
TOPOLOGY: linear  
US-08-627-151A-6

Query Match 100.0%; Score 483; DB 2; Length 6896;

Best Local Similarity 100.0%; Pred. No. 1e-145;

Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1115 AAGTGTGTGTGTCGCAAGGAAATATATGACGCTGAAATGATGATGCTGTACC 1174  
QY 121 TGCAGGAGGTGTGTCGCAAGGAAATATATGACGCTGAAATGATGATGCTGTACC 180  
DB 1175 TGCAGGAGGTGTGTCGCAAGGAAATATATGACGCTGAAATGATGATGCTGTACC 1234  
QY 181 AAGTGTGTGTGTCGCAAGGAAATATATGACGCTGAAATGATGATGCTGTACC 240  
DB 1235 AAGTGTGTGTGTCGCAAGGAAATATATGACGCTGAAATGATGATGCTGTACC 1294  
QY 241 GAGGAGAGGTGTGTCGCAAGGAAATATATGACGCTGAAATGATGATGCTGTACC 300  
DB 1295 GAGGAGAGGTGTGTCGCAAGGAAATATATGACGCTGAAATGATGATGCTGTACC 1354  
QY 301 TGCAGGAGGTGTGTCGCAAGGAAATATATGACGCTGAAATGATGATGCTGTACC 360  
DB 1355 TGCAGGAGGTGTGTCGCAAGGAAATATATGACGCTGAAATGATGATGCTGTACC 1414  
QY 361 AAGGAGAGGTGTGTCGCAAGGAAATATATGACGCTGAAATGATGATGCTGTACC 420  
DB 1415 AAGGAGAGGTGTGTCGCAAGGAAATATATGACGCTGAAATGATGATGCTGTACC 1474  
QY 421 TGCAGGAGGTGTGTCGCAAGGAAATATATGACGCTGAAATGATGATGCTGTACC 480  
DB 1475 TGCAGGAGGTGTGTCGCAAGGAAATATATGACGCTGAAATGATGATGCTGTACC 1534  
QY 481 AAT 483

Db 1535 AAT 1537

Search completed: January 6, 2003, 01:15:08  
Joo time : 70 secs





	Matches	483;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
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Db	1	GATG	TGTGTG	TGCCCCAAGAAATAATAT	W	CAACCCCTCAAAAATAT	T	TGATG	TGCTGTACC	60
Oy	61	AAGTGC	CAACAAAGAACTACTTGT	TACATGACTGT	CC	CGGAGGCAGATAT	ACGAC			120
Db	61	AAGTGC	CAACAAAGAACTACTTGT	TACATGACTGT	CC	CGGAGGCAGATAT	ACGAC			120
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Db	181	AGCTG	CTCCAAATGCGAAAGGAAATG	GGGTCA	GGTGAGATCTTCTT	TTGACACATGGAC				240
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Oy	301	TTCCAG	TGCTTCAATTGCAAGCTCTTGCTCT	CAATGGAGACCGTGCA	CTCTCTCCACAGAG					360
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RESULT 3
US-09-792-356-3
; Sequence 3, Application US/09792356
; Publication No. US20020183485A1
; GENERAL INFORMATION:
; APPLICANT: Hauptmann, Rudolph
; APPLICANT: Himmler, Adolph
; APPLICANT: Maurer-Fogy, Ingrid
; APPLICANT: Stratowa, Christian
; TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for
; FILE OF INVENTION: Them
; FILE REFERENCE: 98,385-G
; CURRENT APPLICATION NUMBER: US/09/792,356
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 08/477,639
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 08/383,676
; PRIOR FILING DATE: 1995-02-01
; PRIOR APPLICATION NUMBER: 08/453,287
; PRIOR FILING DATE: 1993-11-17
; PRIOR APPLICATION NUMBER: 07/821,750
; PRIOR FILING DATE: 1992-01-02
; PRIOR APPLICATION NUMBER: 07/511,430
; PRIOR FILING DATE: 1990-04-20
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 463
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(483)
US-09-792-356-3

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Query Match      100.0%; Score 483; DB 9; Length 483;
Best Local Similarity 100.0%; Pred. No. 2.2e-148;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 GATATGTTGTCCTCCCAAGGAAAATATATCCACCCCTCAAAATAATTCGATTGCTGACC 60

QY 61 AAGTGCACAAAGGAACTACTTGTACATGCTCCAGGCGCCGGGCGAGGATACGGAC 120
DB 61 AAGTGCACAAAGGAACTACTTGTACATGCTCCAGGCGCCGGGCGAGGATACGGAC 120

QY 121 TGCAGGAGATTTGAGAGGCGTTCCTTCCACCGCTTCAGAAAAACCCCTCAGACACTGCGTC 180
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QY 181 AGCTGCTCCAAATGCGGAAAGAAATGAGTGGTACGATGCTCTTCTTGGACAGTGGAC 240
DB 181 AGCTGCTCCAAATGCGGAAAGAAATGAGTGGTACGATGCTCTTCTTGGACAGTGGAC 240

QY 241 CGGACACCCGTTGAGTGGTGGAGGAAAGCAAGTACCGGCAATTTGGAGTGAAGACCTT 300
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QY 301 TTCCAGTCTTCAATTTGAGGCTTCTGCTCAATGGGACCGTGCACCTCTCTCGCCAGGAG 360
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QY 481 AAT 483
DB 481 AAT 483
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RESULT 4
US-09-899-422-3
; Sequence 3, Application US/09899422
; Patent No. US2002090676A1
; GENERAL INFORMATION:
; APPLICANT: Hauptmann, Rudolph
; APPLICANT: Himmeler, Adolph
; APPLICANT: Maurer-Fody, Ingrid
; APPLICANT: Stratowa, Christian
; TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for
; TITLE OF INVENTION: Them
; FILE REFERENCE: 98,385-H
; CURRENT APPLICATION NUMBER: US/09/899,422
; CURRENT FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: 09/525,998
; PRIOR FILING DATE: 2000-03-15
; PRIOR APPLICATION NUMBER: 09/383,676
; PRIOR FILING DATE: 1995-02-01
; PRIOR APPLICATION NUMBER: 08/153,287
; PRIOR FILING DATE: 1993-11-17
; PRIOR APPLICATION NUMBER: 07/821,750
; PRIOR FILING DATE: 1992-01-02
; PRIOR APPLICATION NUMBER: 07/511,430
; PRIOR FILING DATE: 1990-04-20
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 483
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
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NAME/KEY: CDS
LOCATION: (1) (483)
US-09-899-422-3

Query Match      100.0%; Score 483; DB 10; Length 483;
Best Local Similarity 100.0%; Pred. No. 2.2e-148;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GATATGTTGTCCTCCCAAGGAAAATATATCCACCCCTCAAAATAATTCGATTGCTGACC 60
DB 1 GATATGTTGTCCTCCCAAGGAAAATATATCCACCCCTCAAAATAATTCGATTGCTGACC 60

QY 61 AAGTGCACAAAGGAACTACTTGTACATGCTCCAGGCGCCGGGCGAGGATACGGAC 120
DB 61 AAGTGCACAAAGGAACTACTTGTACATGCTCCAGGCGCCGGGCGAGGATACGGAC 120

QY 121 TGCAGGAGATTTGAGAGGCGTTCCTTCCACCGCTTCAGAAAAACCCCTCAGACACTGCGTC 180
DB 121 TGCAGGAGATTTGAGAGGCGTTCCTTCCACCGCTTCAGAAAAACCCCTCAGACACTGCGTC 180

QY 181 AGCTGCTCCAAATGCGGAAAGAAATGAGTGGTACGATGCTCTTCTTGGACAGTGGAC 240
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QY 241 CGGACACCCGTTGAGTGGTGGAGGAAAGCAAGTACCGGCAATTTGGAGTGAAGACCTT 300
DB 241 CGGACACCCGTTGAGTGGTGGAGGAAAGCAAGTACCGGCAATTTGGAGTGAAGACCTT 300

QY 301 TTCCAGTCTTCAATTTGAGGCTTCTGCTCAATGGGACCGTGCACCTCTCTCGCCAGGAG 360
DB 301 TTCCAGTCTTCAATTTGAGGCTTCTGCTCAATGGGACCGTGCACCTCTCTCGCCAGGAG 360

QY 361 AAACACAAATGATGAGGAGGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 420
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QY 421 TCTGTGTAATGATGAGGAGGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 480
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QY 481 AAT 483
DB 481 AAT 483
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RESULT 5
US-09-907-263-1
; Sequence 1, Application US/09907263
; Patent No. US2002011924A1
; GENERAL INFORMATION:
; APPLICANT: Bendelle, Alison M.
; APPLICANT: Sennello, Regina M.
; APPLICANT: Edwards, Carl K.
; TITLE OF INVENTION: PROTEIN FOR TREATING THE MEDIATELY LATE PHASE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 DeHavilland Drive
; CITY: Thousand Oaks
; STATE: CA
; COUNTRY: US
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/907,263
; FILING DATE: 17-Jul-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
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Mon Jan 6 08:48:16 2003

us-09-882-735-1.rnpb

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Page 10

GenCore version 5.1.3  
Copyright (c) 1991 - 2003 CompuGen Ltd.

Genomic nucleic acid - nucleic search, using sw model

Run on: January 6, 2003, 01:15:13, Search time 2255 Seconds  
(without alignments)  
3515.694 Million cell updates/sec

Title: US-09-882-735-1

Perfect score: 483

Sequence: 1 gatagtgtgtccccaagg

Scoring table: IDENTITY NUC .....gctaccacagattgagaat 483

Gapop 10<sup>-6</sup>, Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: EST:

- 1: em\_estba:\*
- 2: em\_esthum:\*
- 3: em\_estin:\*
- 4: em\_estmu:\*
- 5: em\_estov:\*
- 6: em\_estpl:\*
- 7: em\_estro:\*
- 8: em\_hic:\*
- 9: gb\_est1:\*
- 10: gb\_est2:\*
- 11: gb\_hic:\*
- 12: gb\_est3:\*
- 13: gb\_est4:\*
- 14: gb\_est5:\*
- 15: em\_estfun:\*
- 16: em\_estom:\*
- 17: gb\_gss:\*
- 18: em\_gss\_hum:\*
- 19: em\_gss\_inv:\*
- 20: em\_gss\_pln:\*
- 21: em\_gss\_vrt:\*
- 22: em\_gss\_fun:\*
- 23: em\_gss\_mam:\*
- 24: em\_gss\_mus:\*
- 25: em\_gss\_other:\*
- 26: em\_gss\_pro:\*
- 27: em\_gss\_rtd:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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3	483	100.0	974	12	BG180101
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5	481.4	99.7	837	9	AL522989
6	480.4	99.5	1070	13	BM546826

7	471.6	97.6	994	14	BM800044
8	467.6	96.8	975	9	AL577008
9	466.2	96.5	818	13	BI821169
10	457.6	94.7	942	9	AL529836
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12	448.4	92.8	859	13	BI870917
13	444.4	92.0	845	9	AU125021
14	441	91.3	872	13	BI769626
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23	409.4	84.8	1008	14	BQ719773
24	407.6	84.4	951	14	BQ882704
25	406.8	84.2	817	9	AU155689
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27	399.8	82.8	929	12	BG677121
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DEFINITION AGENCOURT 8489850 Lupeki dorsal root ganglion Homo sapiens cDNA  
Clone IMAGE:6184295 5', mRNA sequence.

ACCESSION BQ723672

VERSION BQ723672.1 GI:21862569

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 931)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: [cgapbs-f@mail.nih.gov](mailto:cgapbs-f@mail.nih.gov)

Tissue Procurement: Dr. James R. Lupski

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

CDNA Sequencing by: Agencourt Bioscience Corporation

CDNA distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LHAM33573 row, d column, 24

High quality sequence stop: 607.

FEATURES

Location/Qualifiers 1 931





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 Db 462 TTCCAGAGCGCTGATATGGAGAGGCTCTCTCCACATGGAGACGGTGCATCTCTCTGGAGAG 541  
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 Db 542 AAAACAGAAACCGCTGTGACCTGGACCTGACAGCTTCTCTCTTAAGAGAAAAAGAGTGTCTC 601  
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 Db 662 AAT 664

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LOCUS	
DEFINITION	837 bp cDNA clone CSDB009YP14 5
ACCESSION	AF522989
VERSION	AF522989.1
KEYWORDS	EST.
SOURCE	human,

REFERENCE	TITLE	AUTHORS	COMMENT
Eukaryota; Metazoa; Chordata; Cranata; Vertebrata; Euteleostomi	Mammalia; Eutheria; Primates; Carnivori; Homidae; Homo.	Li W.B., Gruber C., Jessup J. and Polyes D.	Full-length cDNA libraries and normalization
1 (bases 1 to 937)	Capitulum (2001)		Contact: Genoscope

BP 191 91006 EVRY cedex - France  
Email: [segref@genoscope.cns.fr](mailto:segref@genoscope.cns.fr), Web : [www.genoscope.cns.fr](http://www.genoscope.cns.fr)  
Location/Qualifiers

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/clone_1ib="LTI_NFL004_NBC2"
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/lab host="DH10B"
/note="Organ: brain; Vector: PCWMSPORT 6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the PCWMSPORT 6
vector. Library was normalized. Library was constructed
by Life Technologies. Contact : Feng liang life
Technologies, a division of Invitrogen 9800 Medical Center
Drive Rockville, Maryland 20850, USA Fax : (1) 301 610
8371 Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"

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BASE COUNT	199 a	231 c	229 g	177 e	1 others
ORIGIN					

Query Match	99.7%;	Score 481.4;	DB 9;	Length 837;
Best Local Similarity	99.9%;	Pred. No. 2e-142;		
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				Gaps 0;

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[illegible]

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AGENE	6491128 NIH_MGC_125 Homo sapiens	linear CDNA clone IMAGE:5723557
DEFINITION	5', mRNA sequence.	
ACCESSION	BMS546826	
VERSION	BMS546826.1	GI:18780096
KEYWORDS	EST.	
SOURCE	human.	

ORGANISM Homo sapiens  
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi  
Mammalia, Eutheria, Primates, Catarrhini, Hominoidea, Homo.  
1 (bases 1 to 1070)  
REFERENCE NIH-MGC <http://mgc.nci.nih.gov/>.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.

FEATURES

Tissue Procurement:	Invitrogen
cDNA Library Preparation:	Life Technologies, Inc.
cDNA Library Arrayed by:	The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by:	Agencourt Bioscience Corporation
Clone distribution:	MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <a href="http://image.llnl.gov">http://image.llnl.gov</a>
Plate:	L96ML11 row, g column: 14
High quality sequence start:	2
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Location/Qualifiers	

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/clone_id="NH_MGC_125"
/lab_host="DH10B"
/note="Organ: ovary (pool of 3); Vector: pCMV-Sport6;
Site 1: EcoRV (destroyed); Site 2: NotI; RNA source pool
of three ovaries; from females ranging in age from 38 to
49 yo. Library is oligo-dT primed and directionally cloned
(EcoRV site is destroyed upon cloning). Average insert
size 2.1 kb, insert size range 1.3-5 kb. Library is
normalized and enriched for full-length clones and was
constructed by C. Gruber (Invitrogen). Research Genetics
tracking code 036."

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BASE COUNT      241 a   311 c   293 g   224 t       1 others
ORIGIN

Query Match      99.58; Score 480.4; DB 13; Length 1070;
Best Local Similarity 99.28; Pred. No. 5e-142;
Matches 481; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GATAGTGTGTGTCGCCAAGGAAATATATGACGCTTCAAAATATTCGATTCGTGTACC 60
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QY 61 AAGTCCCAAGGAAATATATGACGCTTCAAAATATTCGATTCGTGTACC 120
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DB 506 AGCTGCTCCAAATGCGGAAAGGAAATGCGGTCAGGTGGAGATCTCTTCTGCACAGTGGAC 565

QY 241 CGGACACCGGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
DB 626 TCCAGTGTCTCAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAAT 685

QY 361 AAAGACACCGGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
DB 686 AAAGACACCGGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 745

QY 421 TCCAGTGTCTCAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAAT 480
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QY 481 AAT 483
DB 806 AAT 808

RESULT: 7
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LOCUS      AGENCOURT 6415909 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:5531041
DEFINITION 5' mRNA sequence.
ACCESSION  RM800044
VERSION     RM800044.1 GI:19116867
KEYWORDS   EST.
SOURCE      human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  NIH-MGC http://mgi.nci.nih.gov/.
            National Institutes of Health, Mammalian Gene Collection (MGC)
            Unpublished (1999)
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-remail.nih.gov
            Tissue Procurement: ATCC
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I M A G E Consortium (ILNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/ILNL at:
            http://image.llnl.gov
            Plate: ILNL212 row. b column: 62
            High quality sequence stop: 654.
            Location/Qualifiers
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Site 2: Salt; Cloned unidirectionally. Primers: clone 47.
Average insert size 2.1 kb."
BASE COUNT      233 a   284 c   262 g   212 t       3 others
ORIGIN

Query Match      97.68; Score 471.6; DB 14; Length 944;
Best Local Similarity 99.28; Pred. No. 3.1e-139;
Matches 474; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GATAGTGTGTGTCGCCAAGGAAATATATGACGCTTCAAAATATTCGATTCGTGTACC 60
DB 286 GATAGTGTGTGTCGCCAAGGAAATATATGACGCTTCAAAATATTCGATTCGTGTACC 445

QY 61 AAGTCCCAAGGAAATATATGACGCTTCAAAATATTCGATTCGTGTACC 120
DB 346 AAGTCCCAAGGAAATATATGACGCTTCAAAATATTCGATTCGTGTACC 400

QY 121 TCAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAAT 180
DB 406 TCAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAAT 465

QY 181 AGCTGCTCCAAATGCGGAAAGGAAATGCGGTCAGGTGGAGATCTCTTCTGCACAGTGGAC 240
DB 466 AGCTGCTCCAAATGCGGAAAGGAAATGCGGTCAGGTGGAGATCTCTTCTGCACAGTGGAC 526

QY 241 CGGACACCGGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
DB 526 CGGACACCGGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 386

QY 301 TCCAGTGTCTCAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAAT 400
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QY 361 AAAGACACCGGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
DB 646 AAAGACACCGGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 706

QY 421 TCCAGTGTCTCAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAAT 478
DB 706 TCCAGTGTCTCAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAAT 764

RESULT 8
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LOCUS      AL577008 LTI_NFL006 PL2 Homo sapiens cDNA clone CS001087YAG1.5
DEFINITION prime, mRNA sequence.
ACCESSION  AL577008
VERSION     AL577008.1 GI:12909716
KEYWORDS   EST.
SOURCE      human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  Li, W. H., Gruber, C., Jassby, J. and Polayes, D.
            Full-length cDNA libraries and normalization
            Unpublished (2001)
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 Evry cedex - France
            Email: segre@genoscope.cns.fr, Web : www.genoscope.cns.fr.
            Location/Qualifiers
            source      1. .975
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RESULT 10  
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LOCUS  
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prime, mRNA sequence.  
ACCESSION AL529816  
VERSION AL529816.1 GI:12743329  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 942)  
AUTHORS Li, W.B., Gruber, C., Jesse, J. and Polayes, D.  
TITLE Full-length cDNA libraries and normalization  
JOURNAL Unpublished (2001)  
COMMENT Contact: Genoscope  
Genoscope, Centre National de Sequencage  
HP 191 91006 EVRY cedex - France  
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr.  
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1..942  
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/clone="CSDD0005YP05"  
/sex="male"  
/tissue\_type="neuroblastoma cells"  
/lab\_host="DH10B"  
/note="Organ: brain, Vector: pCMVSPORT 6; 1st strand cDNA  
was primed with a NotI-oligo(dT) primer. Five prime end  
enriched, double-stranded cDNA was digested with Not I and  
cloned into the Not I and Eco RV sites of the pCMVSPORT 6  
vector. Library was normalized. Library was constructed  
by Life Technologies. Contact: Feng Liang Life  
Technologies, a division of Invitrogen 9800 Medical Center  
Drive Rockville, Maryland 20850, USA Fax: (1) 301 610  
8371 Email: fliang@lifetech.com  
http://fulllength.invitrogen.com"  
BASE COUNT 208 a 259 c 248 g 224 t 3 others  
ORIGIN  
Query Match 94.7%; Score 457.6; DB 9; Length 942;  
Best Local Similarity 99.2%; Pred. No. 4 9a-115;  
Matches 480; Conservative 1; Mismatches 1; Indels 2; Gaps 2;  
QY 1 GATAGTGTGTGTCCTCCCAAGGAAATATATCCACCCCTCAAAATAATTCGATTGCTGTACC 60  
DB 354 GATAGTGTGTGTCCTCCCAAGGAAATATATCCACCCCTCAAAATAATTCGATTGCTGTACC 413  
QY 61 AAGTGGCAAAAGGAACCTACTTGTACAAATGACTGTCCAGCCCGGGGCGAGGATACGGAC 120  
DB 414 AAGTGGCAAAAGGAACCTACTTGTACAAATGACTGTCCAGCCCGGGGCGAGGATACGGAC 473  
QY 121 TGAGAGGATATGAG 180  
DB 474 TGAGAGGATATGAG 533  
QY 181 AGCTGCTTCAAAATGTCGAG 240  
DB 534 AGCTGCTTCAAAATGTCGAG 593  
QY 241 CGAG 300  
DB 594 CGAG 653  
QY 361 TTCCAG 360  
DB 654 TTCCAG 713  
QY 361 AAAAG 419  
DB 714 AAAAG 773

QY 420 CTCCTGTAGTAACTGTAGAGAAAGCTGTAGAGAAATTTTGTGTTTATATATATATATAT 479  
DB 774 CTCCTGTAGTAACTGTAGAGAAAGCTGTAGAGAAATTTTGTGTTTATATATATATATAT 840  
QY 480 GAAT 483  
DB 833 GAAT 836  
RESULT 11  
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LOCUS  
DEFINITION BB871809 NIH\_MGC\_65 Homo sapiens cDNA clone IMAGE486296 5',  
mRNA sequence.  
ACCESSION BB871809  
VERSION BB871809.1 GI:10320585  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 969)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cga@frcmail.nih.gov  
Tissue Procurement: ATCC  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNLI)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/ILNLI at:  
http://image.llnl.gov  
Plate: LHAM9574 row: o column: 22  
High quality sequence stop: 642.  
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1..969  
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Site 2: SalI; Cloned unidirectionally. Primers: oligo dT.  
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Technologies."  
BASE COUNT 281 a 273 c 241 g 174 t  
ORIGIN  
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Best Local Similarity 99.6%; Pred. No. 1 9e-132;  
Matches 462; Conservative 0; Mismatches 1; Indels 1; Gaps 1;  
QY 21 AAAATATATATCCAC-CCTCAAAATAATTCGATTGCTGTGTTTATATATATATATATAT 79  
DB 1 AAAATATATATCCACCTCAAAATAATTCGATTGCTGTGTTTATATATATATATATATAT 60  
QY 80 ACTTGTACAAATGATCTGTGAG 149  
DB 61 ACTTGTACAAATGATCTGTGAG 128  
QY 140 GCTCTCTTCCAGGCTTCCAGGAAAGAAATATATATATATATATATATATATATATATAT 199  
DB 121 GCTCTCTTCCAGGCTTCCAGGAAAGAAATATATATATATATATATATATATATATATAT 140  
QY 250 AGGAAATGAGTGTGAG 269  
DB 181 AGGAAATGAGTGTGAG 240  
QY 260 CCAG 419

Query Match:	92.0%	Score 444.4	EB 3	Length 845
Best Local Similarity	99.2%	Pred. No. 1.4e-130		
Matches 457	Conservative 0	Mismatches 2	Indels 2	Gaps 2

QY 1 GAGAGTGTGTGCCAAGAAATATATCCACCCCTCAAAATATATCATTTGCTGTAAC 60



HRI human cDNA project, 5'- & 3'-end one pass sequencing: Helix  
Research Institute/ cDNA library construction: Department of  
Virology, Institute of Medical Science, University of Tokyo, and  
Helix Research Institute.

## FEATURES

Source

Location/Qualifiers

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/clone="NT2RM400018"  
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/cell\_type="teratocarcinoma"  
/cell\_line="NT2"  
/note="Vector: pWESF13; mRNA from uninduced NT2 neuronal  
precursor cells"

BASE COUNT 127 a 247 c 220 g 192 t 3 others

ORIGIN

Query Match

30.54; Score 439; DB 9; Length 859;

Best Local Similarity 98.1%; Pred. No. 7,4e-129;

Matches 453; Conservative 0; Mismatches 8; Indels 1; Gaps 1,

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UY 1  GATAGTGTGTGTCCTCCAGGAAATATATCCACCTCAAAATATTCGATTGCTGTACC 60
DB 399 GATAGTGTGTGTCCTCCAGGAAATATATCCACCTCAAAATATTCGATTGCTGTACC 458
UY 41  AAGGCTGCAAGCAACCTTCTTATATCTGTGTGAGGCTGAGGCTGAGGCTGAGGCT 120
DB 409 AAGGCTGCAAGCAACCTTCTTATATCTGTGTGAGGCTGAGGCTGAGGCTGAGGCT 518
UY 121  TCCAGGAGAGTGTGAGGAGGCTGCTTCAAGGCTTCAAGGAGGCTGAGGCTGAGGCTG 180
DB 519 TCCAGGAGAGTGTGAGGAGGCTTCTTCAAGGCTTCAAGGAGGCTGAGGCTGAGGCT 578
UY 181  AAGTGTCTCAATGCGGAAAGGAAATGCGGTGAGGATCTCTTCTGCAACAGTGGAC 240
DB 579 AAGTGTCTCAATGCGGAAAGGAAATGCGGTGAGGATCTCTTCTGCAACAGTGGAC 638
UY 241  CAGGAGAGTGTGAGGAGGCTGAGGAGGCTGAGGAGGCTGAGGAGGCTGAGGAGGCT 300
DB 639 CAGGAGAGTGTGAGGAGGCTGAGGAGGCTGAGGAGGCTGAGGAGGCTGAGGAGGCT 698
UY 301  TCCAGGAGAGTGTGAGGAGGCTGAGGAGGCTGAGGAGGCTGAGGAGGCTGAGGAGG 360
DB 699 TCCAGGAGAGTGTGAGGAGGCTGAGGAGGCTGAGGAGGCTGAGGAGGCTGAGGAG 757
UY 361  AAGGAGAGTGTGAGGAGGCTGAGGAGGCTGAGGAGGCTTCTTCTGAGGAGGAGGCT 420
DB 759 AAGGAGAGTGTGAGGAGGCTGAGGAGGCTGAGGAGGCTTCTTCTGAGGAGGAGGCT 817
UY 421  TCCAGGAGAGTGTGAGGAGGCTGAGGAGGCTGAGGAGGCTGAGGAGGCTGAGGAG 480
DB 817 TCCAGGAGAGTGTGAGGAGGCTGAGGAGGCTGAGGAGGCTGAGGAGGCTGAGGAG 876

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Search completed: January 6, 2003, 03:39:59  
Job time : 2254 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

tm protein - protein search, using sw model

Run on: January 6, 2003, 03:45:53, Search time 33 seconds  
(without alignments)  
650.102 Million cell updates/sec

Title: US-09-882 735-2

Perfect score: 941

Sequence: 1 GSVCPQGYHHPQNNSSHT CSNFFYSLEKTKLQIPQHN 161

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 908470 seqs, 13250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Data base: A Geneseq 101002.\*

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- 2: /SID52/qcgdata/geneseq/geneseq-emb1/AA1981.DAT.\*
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- 22: /SID52/qcgdata/geneseq/geneseq-emb1/AA2001.DAT.\*
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Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	941	100.0	161	11	AA27496 Native 30 kD TNF i
2	941	100.0	161	19	AAW59664 Human soluble tumo
3	941	100.0	161	19	AAW52267 Soluble tumour nec
4	941	100.0	161	20	AAW69233 Tumour necrosis in
5	941	100.0	161	22	AAW37676 Human 30 kDa TNF i
6	941	100.0	211	20	AAW89225 Tumour necrosis fa
7	941	100.0	280	22	AAW66976 Tnfri protein. Un
8	941	100.0	309	16	AAW70108 TNF-R-G8PH fusion
9	941	100.0	311	20	AAW89229 Tumour necrosis fa
10	941	100.0	336	18	AAW33360 TBP(20-190)/hcg-be

11	941	100.0	366	20	AAW89228 Tumour necrosis fa
12	941	100.0	371	11	AAW07449 Tumour necrosis fa
13	941	100.0	377	20	AAW89227 Tumour necrosis fa
14	941	100.0	417	20	AAW89226 Tumour necrosis fa
15	941	100.0	420	20	AAW89224 Tumour necrosis fa
16	941	100.0	451	16	AAW70107 TNF R GRP 140 fusi
17	941	100.0	455	12	AAW10986 30kD TNF inhibitor
18	941	100.0	455	12	AAW11082 Human 30kD TNF bin
19	941	100.0	455	13	AAW20787 TNF alpha binding
20	941	100.0	455	13	AAW24000 TNF alpha ccd. rec
21	941	100.0	455	14	AAW42059 Lambda derived TNF
22	941	100.0	455	16	AAW50884 p55 TNF R. Bm. p
23	941	100.0	455	20	AAW30934 Human tumour necro
24	941	100.0	455	21	AAW36266 Human tumour necro
25	941	100.0	455	21	AAW37800 Human tumour necro
26	941	100.0	455	21	AAW26984 Human TNFR 1. Hom
27	941	100.0	455	21	AAW23446 Human tumour necro
28	941	100.0	455	21	AAW01336 TNF R. death recep
29	941	100.0	455	22	AAW86817 Human TNFRP associ
30	941	100.0	455	22	AAW36697 Human tumour necro
31	941	100.0	455	22	AAW37677 Human 40 kDa TNF 1
32	941	100.0	455	23	AAW81649 Human tumour necro
33	941	100.0	455	23	AAW75064 Human tumour necro
34	941	100.0	547	16	AAW70104 TNF R GRP fusion
35	941	100.0	884	16	AAW70109 TNF R GRP 140 fusi
36	941	100.0	900	16	AAW70103 TNF R GRP 140 fusi
37	941	100.0	1245	16	AAW70106 TNF R p1. vlvax fu
38	941	100.0	1604	16	AAW70105 TNF R ERA 176 fusi
39	938	99.7	455	11	AAW07451 Human Tumour Necro
40	932	99.0	433	14	AAW51032 Mutant p55 tumour
41	932	99.0	443	14	AAW51033 p55 Tumour necrosi
42	932	99.0	455	14	AAW42197 Mutant p55 tumour
43	932	99.0	455	14	AAW51034 Mutant p55 tumour
44	931	98.9	455	12	AAW12550 Type 1 TNF receptor
45	930.5	98.9	909	19	AAW64485 Human Fas protein.

ALIGNMENTS

RESULT 1  
AAW27496  
ID AAW27496 standard; protein; 161 AA.

XX AAW27496;

XX 09-MAR-1993 (first entry)

XX Native 30 kD TNF inhibitor.

XX Tumour necrosis factor; ethylene glycol; pharmacokinetic;

XX adult respiratory distress syndrome; rheumatoid arthritis;

XX septic shock; pulmonary fibrosis; spacer.

XX Homo sapiens

XX WQ9216221-A.

XX 01-OCT-1992.

XX 13 MAR-1992; 92WO-US02122.

XX 15-MAR-1991; 91US-0669662

XX 17-JAN 1992; 92US-0822296.

XX (SYND ) SYNERGEN INC.

XX Arnes LG, Brewer MT, Evans PJ, Kohno T, Thompson RC;

XX WFI, 1992-348933/42.

XX New ethylene glycolated polypeptide(s) with improved

XX pharmacokinetic properties - for treating e.g. TNF and IL-1

mediated diseases, e.g. adult respiratory distress syndrome, rheumatoid arthritis, septic shock etc.

Claim 54; Fig 2; 100pp; English.

The sequence shows a native 30 kD TNF inhibitor which may be modified to contain at least one non-native cysteine residue, pref. at positions 1, 14, 105, 111 and/or 165. The non-native cysteine is joined to a non-peptidic polymer, pref. monomethoxy PEG via thio-ether bonds. Two such TNF inhibitor mols. may be linked via this non-peptidic spacer. The modified polypeptides show improved pharmacokinetic properties, i.e. increased mol. wt. hence reduced clearance rate following s.c. or systemic administration, increased sol. of native TNF inhibitors, and reduced antigenicity. The polypeptides may be used for treatment of TNF mediated diseases such as adult respiratory distress syndrome, pulmonary fibrosis, rheumatoid arthritis, inflammatory bowel disease and septic shock. The same method may be applied to the interleukin-1 receptor antagonist IL-1ra. See also AAR27495.

Sequence 161 AA;

Query Match 100.0%; Score 941; DB 13; Length 161;  
Best Local Similarity 100.0%; Pred. No. 2,4e-67;  
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 DSVCPGKGIHPQNNSTICTCKHKGTYLVNDCPGPDIDDCRECSGFTASENHLRHCL 60  
1 DSVCPGKGIHPQNNSTICTCKHKGTYLVNDCPGPDIDDCRECSGFTASENHLRHCL 60  
1 SCSCRKEMQVEISSCTVDRTVCGCRKNQYRWYSENLFOCFNCSLCINGTVHLSQCE 120  
1 SCSCRKEMQVEISSCTVDRTVCGCRKNQYRWYSENLFOCFNCSLCINGTVHLSQCE 120  
1 KONTVCTCHAGFFLENECVSCSNCKKSLLECTKLCUPOIEN 161  
1 KONTVCTCHAGFFLENECVSCSNCKKSLLECTKLCUPOIEN 161

#### RESULT 2

AAW59664 standard; Protein; 161 AA.

AAW59664;

28-SEP-1998 (first entry)

Human soluble tumour necrosis factor receptor type I.

Human; tumour necrosis factor; TNF; TNF receptor type I;

inflammatory disease; leukaemia; TNF binding protein;

anti-inflammatory drug; methotrexates.

Homo sapiens.

MO9824463-A2.

11-JUN-1998.

08-DEC-1997; 97WO-US22733.

09-JUN-1997; 97US-0052023.

06-DEC-1996; 96US-0032587.

23-JAN-1997; 97US-0036355.

07-FEB-1997; 97US-0039315.

(AMGE-) AMGEN INC.

Bendele AM, Edwards CK, Sennello RM;

WP1; 1998-333039/29.

N-PSDB; AAW41548.

Treatment of acute or chronic inflammatory disease, e.g. leukaemia - by administering tumour necrosis factor binding protein and at least one additional anti-inflammatory drug, e.g. methotrexate

Disclosure; Fig 1; 104pp; English.

This is the amino acid sequence of the human tumour necrosis factor receptor type I, used in the method of the invention involving the treatment of acute or chronic inflammatory disease such as leukaemia by administering tumour necrosis factor binding protein and at least one additional anti-inflammatory drug, e.g. methotrexate.

Sequence 161 AA;

Query Match 100.0%; Score 941; DB 19; Length 161;  
Best Local Similarity 100.0%; Pred. No. 2,4e-67;  
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 DSVCPGKGIHPQNNSTICTCKHKGTYLVNDCPGPDIDDCRECSGFTASENHLRHCL 60  
1 DSVCPGKGIHPQNNSTICTCKHKGTYLVNDCPGPDIDDCRECSGFTASENHLRHCL 60  
1 SCSCRKEMQVEISSCTVDRTVCGCRKNQYRWYSENLFOCFNCSLCINGTVHLSQCE 120  
1 SCSCRKEMQVEISSCTVDRTVCGCRKNQYRWYSENLFOCFNCSLCINGTVHLSQCE 120  
1 KONTVCTCHAGFFLENECVSCSNCKKSLLECTKLCUPOIEN 161  
1 KONTVCTCHAGFFLENECVSCSNCKKSLLECTKLCUPOIEN 161

#### RESULT 3

AAW52267 standard; Protein; 161 AA.

AAW52267;

29-JUN-1998 (first entry)

Soluble tumour necrosis factor receptor.

Soluble tumour necrosis factor receptor; sTNF; TNF-mediated disease;

tumour necrosis factor binding protein; autoimmune disease; arthritis;

adult respiratory distress syndrome; cachexia/anorexia; cancer; therapy;

chronic fatigue syndrome; graft rejection; Alzheimer's disease; TNBP.

Homo sapiens.

MO9801555-A2.

15-JAN-1998.

09-JUL-1997; 97WO-US12244.

04-MAR-1997; 97US-0039792.

09-JUL-1996; 96US-0021443.

06-DEC-1996; 96US-0032534.

23-JAN-1997; 97US-0037737.

07-FEB-1997; 97US-0039314.

(AMGE-) AMGEN INC.

Edwards CK, Fisher EF, Kieft GL;

WP1; 1998-101052/09.

N-PSDB; AAV19801.

Truncated and soluble forms of tumour necrosis factor receptor -

useful for treating diseases involving factor, e.g. arthritis and

adult respiratory distress syndrome

Claim 1; Fig 1; 205pp; English.

This sequence is the human soluble tumour necrosis factor receptor (STNFR). The protein was used to make the truncated STNFR proteins of the invention. The truncated STNFR proteins and tumour necrosis factor binding proteins (TNBP) are used to treat any TNF-mediated disease, e.g. arthritis, adult respiratory distress syndrome, cachexia/anorexia, cancer, chronic fatigue syndrome, graft rejection, Alzheimer's disease and other autoimmune diseases. Cells transformed with a vector containing DNA encoding the protein may be used for production of recombinant STNFR, which may also be used for measuring the amount of STNFR in samples and to raise antibodies against STNFR. TNBP may also be used in preparation of therapeutic compositions for treating the above diseases. The STNFR proteins are well suited to large scale production (since they lack the deamidation site in region III-126, so are more stable in vivo); contain fewer disulphide bonds and fewer epitopes, making them less antigenic than full-length proteins.

Query Match 100.0%; Score 941; DR 19; Length 161;  
Best Local Similarity 100.0%; Pred. No. 2.4e-67;  
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSVCPQCKYHPQNNISCTCTCHKGTLYNDCPGPGQDTCPCESSGFTASENHLPHCL 60  
DB 1 DSVCPQCKYHPQNNISCTCTCHKGTLYNDCPGPGQDTCPCESSGFTASENHLPHCL 60

QY 61 SCSKPFEMGQVEISSCTVDPTVCGCPFNQVPHWSENLFQCNCLNGTIVHLSQCE 120  
DB 61 SCSKPFEMGQVEISSCTVDPTVCGCPFNQVPHWSENLFQCNCLNGTIVHLSQCE 120

QY 121 KQNTVCTCHAGFFIENFECVSCNCFKSLCTYLCLPOIEN 161  
DB 121 KQNTVCTCHAGFFIENFECVSCNCFKSLCTYLCLPOIEN 161

RESULT 4  
AAB9233  
ID AAB9233 standard; Protein; 161 AA.  
XX AC AAB9233;  
XX DT 04 MAR 1999 (first entry)  
XX DE Tumour necrosis inhibitor 30 kDa protein.  
XX KW Tumour necrosis factor receptor 1, TNFR-1; inhibitor, osteoprotegerin;  
XX KW OPG; chimeric; fusion; dimerisation domain; autoimmune disease;  
XX KW inflammation; apoptosis.  
XX OS Homo sapiens.  
XX PN W09849405.A1.  
XX PD 05-NOV-1998.  
XX PF 29-APR 1998; 98WO-0508631.  
XX PR 01-MAY 1997; 97US-0850188.  
XX PA (AMGE ) AMGEN INC.  
XX PI Boyle WJ, Wooden S;  
XX DR WPI; 1999-034661/03.  
XX DR N-PSDB; AAV81732.  
XX PT New chimeric osteoprotegerin polypeptides - contain the  
XX PT osteoprotegerin dimerisation domain and a heterologous sequence,  
XX PT useful to treat TNF and TNFR-mediated disorders  
XX PS Disclosure; Fig 2; 92pp; English.  
XX PT The present invention describes a chimeric polypeptide (A1), comprising

an osteoprotegerin (OPG) dimerisation domain fused to a heterologous amino acid sequence. Also described are: (1) a multimer polypeptide comprising covalently associated A1 monomers; (2) an isolated nucleic acid encoding A1; (3) an expression vector comprising the nucleic acid sequence; and (4) a host cell transformed or transfected with the expression vector so that the nucleic acid is expressible. The products from the present invention are useful to treat a variety of disorders including those related to receptor binding. Compositions comprising tumour necrosis factor (TNF)/OPG and TNF receptor (TNFR)/OPG chimeras are used to treat TNF and TNFR-mediated disorders such as inflammation, autoimmune diseases and disorders related to excessive apoptosis. The chimeras are also useful for detecting molecules which interact with fused heterologous sequences to identify potential new receptors and ligands. The present sequence represents the TNF inhibitor 30 kDa protein.

Query Match 100.0%; Score 941; DR 20; Length 161;  
Best Local Similarity 100.0%; Pred. No. 2.4e-67;  
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSVCPQCKYHPQNNISCTCTCHKGTLYNDCPGPGQDTCPCESSGFTASENHLPHCL 60  
DB 1 DSVCPQCKYHPQNNISCTCTCHKGTLYNDCPGPGQDTCPCESSGFTASENHLPHCL 60

QY 61 SCSKPFEMGQVEISSCTVDPTVCGCPFNQVPHWSENLFQCNCLNGTIVHLSQCE 120  
DB 61 SCSKPFEMGQVEISSCTVDPTVCGCPFNQVPHWSENLFQCNCLNGTIVHLSQCE 120

QY 121 KQNTVCTCHAGFFIENFECVSCNCFKSLCTYLCLPOIEN 161  
DB 121 KQNTVCTCHAGFFIENFECVSCNCFKSLCTYLCLPOIEN 161

RESULT 5  
AAB37676  
ID AAB37676 standard; protein; 161 AA.  
XX AC AAB37676;  
XX DT 02-MAR-2001 (first entry)  
XX DE Human 30 kDa TNF inhibitor.  
XX KW TNF inhibitor; antiinflammatory, Tumour Necrosis Factor; interleukin;  
XX KW IL-1; inflammatory disease; degenerative disease; human.  
XX OS Homo sapiens.  
XX PN US6143866-A.  
XX PD 07-NOV-2000.  
XX PF 19-JAN-1995; 95US-0375242.  
XX PR 19-JUL-1990; 90US-0555274.  
XX PR 09-JUL-1993; 93US-0090366.  
XX PR 18-JUL-1989; 89US-0381080.  
XX PR 11-DEC-1989; 89US-0450329.  
XX PR 07-FER-1990; 90US-0479661.  
XX PA (AMGE-) AMGEN INC.  
XX PI Squires C, King MW, Hale KK, Brewer MT, Thompson RC;  
XX PI Vanderslice RW, Vannice J, Kohno T;  
XX DR WPI; 2001-006443/01.  
XX DR N-PSDB; AAC83945.  
XX PT Novel 30 kDa tumor necrosis factor inhibitor analog comprising a  
XX PT non-native cysteine residue cross linked with polyethylene glycol,  
XX PT useful for treating inflammatory and degenerative diseases mediated by

PT TNF -  
 XX Claim 1; Fig 19; 82pp; English.  
 XX  
 CC The present invention relates to Tumour Necrosis Factor (TNF) inhibitors  
 CC (see AAB37676 and AAB37685), which have TNF inhibitory activity. The  
 CC novel TNF inhibitors of the present invention are useful as therapeutic  
 CC agents for inhibiting the activity of TNF and interleukin (IL-1), and  
 CC for treating inflammatory and degenerative diseases mediated by TNF. The  
 CC 30 kDa TNF inhibitor can inhibit TNF alpha  
 CC  
 SQ Sequence 161 AA;  
 Query Match 100.0%; Score 941; DB 22; Length 161;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-67;  
 Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 UY 1 DSVCPGKRYIHPNNNSICTCKHKGYLYNDGPGQDDDCRCESGFTASENHLRHCL 60  
 DB 1 DSVCPGKRYIHPNNNSICTCKHKGYLYNDGPGQDDDCRCESGFTASENHLRHCL 60  
 CY 61 SCSKCKREMGGVEISCTVDRDITVCGCRKQYRHYSENLFQCFNCSLCLNGTVHLSCE 120  
 DB 61 SCSKCKREMGGVEISCTVDRDITVCGCRKQYRHYSENLFQCFNCSLCLNGTVHLSCE 120  
 CY 121 KQNTVCTCHAGFFURENECVSCNCKKSLCTKLCIPQIEN 161  
 DB 121 KQNTVCTCHAGFFURENECVSCNCKKSLCTKLCIPQIEN 161  
 RESULT 6  
 AAB89225  
 ID AAB89225 standard; Protein; 211 AA.  
 AC AAB89225;  
 DT 04-MAR-1999 (first entry)  
 XX  
 DE Tumour necrosis factor b2/osteoprotegerin construct TNFbp 4.0.  
 XX  
 KW Tumour necrosis factor receptor 1; TNFR-1; inhibitor; osteoprotegerin;  
 KW OPG; chimeric; fusion; dimerisation domain; autoimmune disease;  
 KW inflammation; apoptosis.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 PN WO9849305-A1.  
 XX  
 PD 05-NOV-1998.  
 XX  
 PF 29-APR-1999; 98WO-US06631.  
 XX  
 PR 01-MAY-1999; 9/US-0650194  
 XX  
 PA (AMGE-) AMGEN INC.  
 XX  
 PI Boyle WJ, Wooden S;  
 XX  
 DR WPI; 1999-034661/03.  
 XX  
 PT New chimeric osteoprotegerin polypeptides - contain the  
 PT osteoprotegerin dimerisation domain and a heterologous sequence,  
 PT useful to treat TNF and TNFR-mediated disorders  
 XX  
 PS Example 1; Fig 4; 92pp; English.  
 CC The present invention describes a chimeric polypeptide (A1), comprising  
 CC an osteoprotegerin (OPG) dimerisation domain fused to a heterologous  
 CC amino acid sequence. Also described are: (1) a multimer polypeptide  
 CC comprising covalently associated A1 monomers; (2) an isolated nucleic  
 CC acid encoding A1; (3) an expression vector comprising the nucleic acid  
 CC sequence; and (4) a host cell transformed or transfected with the

CC expression vector so that the nucleic acid is expressible. The products  
 CC from the present invention are useful to treat a variety of disorders  
 CC including those related to receptor binding. Compositions comprising  
 CC tumour necrosis factor (TNF)/OPG and TNF receptor (TNFR)/OPG chimeras  
 CC are used to treat TNF and TNFR-mediated disorders such as inflammation,  
 CC autoimmune diseases and disorders related to excessive apoptosis. The  
 CC chimeras are also useful for detecting molecules which interact with  
 CC fused heterologous sequences to identify potential new receptors and  
 CC ligands. The present sequence represents a TNFbp/OPG construct from  
 CC the example of the present invention for creating TNFbp/OPG fusion  
 CC proteins.  
 XX  
 SQ Sequence 211 AA;  
 Query Match 100.0%; Score 941; DB 20; Length 211;  
 Best Local Similarity 100.0%; Pred. No. 3.1e-67;  
 Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 DSVCPGKRYIHPNNNSICTCKHKGYLYNDGPGQDDDCRCESGFTASENHLRHCL 60  
 DB 41 DSVCPGKRYIHPNNNSICTCKHKGYLYNDGPGQDDDCRCESGFTASENHLRHCL 100  
 OY 61 SCSKCKREMGGVEISCTVDRDITVCGCRKQYRHYSENLFQCFNCSLCLNGTVHLSCE 120  
 DB 101 SCSKCKREMGGVEISCTVDRDITVCGCRKQYRHYSENLFQCFNCSLCLNGTVHLSCE 160  
 OY 121 KQNTVCTCHAGFFURENECVSCNCKKSLCTKLCIPQIEN 161  
 DB 161 KQNTVCTCHAGFFURENECVSCNCKKSLCTKLCIPQIEN 201

RESULT 7  
 AAB66979  
 ID AAB66979 standard; Protein; 280 AA.  
 AC AAB66979;  
 DT 19-APR-2001 (first entry)  
 XX  
 DE Tnfr1 protein.  
 XX  
 KW Bone loss; osteoprotegerin; OPG; rheumatoid arthritis; hyperalgesia;  
 KW multiple sclerosis; osteoporosis; osteomyelitis; asthma; inflammation;  
 KW systemic lupus erythematosus; graft-versus-host disease; septic shock;  
 KW acute pancreatitis; Alzheimer's disease; anorexia; atherosclerosis; pain;  
 KW coronary condition; myocardial infarction; cancer; diabetes; psoriasis;  
 KW endometriosis; fever; glomerulonephritis; inflammatory bowel disease;  
 KW ischaemia; Parkinson's disease.  
 XX  
 OS Unidentified.  
 OS  
 XX  
 PN WO200103719-A2.  
 XX  
 PD 18-JAN-2001.  
 XX  
 PF 07-JUL-2000; 2000WO-US18667.  
 XX  
 PR 09-JUL-1999; 99US-0350670.  
 XX  
 ER 09-DEC-1999; 99US-0457647.  
 XX  
 FA (AMGE-) AMGEN INC.  
 XX  
 FI Boyle WJ, Lacey DL, Calzone FU, Chang M, Senaldi G;  
 XX  
 DR WPI; 2001-103031/11.  
 XX  
 PT Treating conditions leading to bone loss such as rheumatoid arthritis,  
 PT multiple sclerosis and asthma, comprises administering an  
 PT osteoprotegerin protein in conjunction with e.g. inhibitors of  
 PT interleukin and tumor necrosis factor alpha  
 XX  
 PS Disclosure; Fig 2; 316pp; English.  
 XX



The present invention relates to a method for treating conditions leading to bone loss. The method comprises administering a purified and isolated osteoprotegerin (OPG) protein (AAF57836-AAF57838 and AAB66974-AAB66976) in conjunction with other substances such as tumour necrosis factor- $\alpha$  (TNF- $\alpha$ ) inhibitors, interleukin (IL)-6, -8 and -18 inhibitors, ICE modulators, fibroblast growth factor (FGF)-10 modulators and/or platelet activating factor (PAF) antagonists. The method is useful for treating conditions leading to bone loss such as rheumatoid arthritis, multiple sclerosis, osteoporosis, osteomyelitis and asthma. The method is also useful for treating inflammation, systemic lupus erythematosus (SLE) and graft-versus-host disease (GVHD). Other diseases that can be treated include acute pancreatitis, Alzheimer's disease, anorexia, atherosclerosis, coronary conditions (e.g. myocardial infarction), cancer, diabetes, endometriosis, fever, glomerulonephritis, hyperalgesia, inflammatory bowel disease, ischaemia, pain, Parkinson's disease, psoriasis and septic shock. The present sequence was used in a sequence homology comparison.

XX Sequence 280 AA;  
 Query Match 100.0%; Score 941; DB 22; Length 280;  
 Best Local Similarity 100.0%; Pred. No. 4e-67;  
 Matches 161, Conservative 0, Mismatches 0, Indels 0, Gaps 0;  
 QY 1 DSVCPQGYIHPQNNISCTCTCHGTYLYNDGCPGPGQDTDCPECSGFTASENHLPCHL 60  
 DB 41 DSVCPQGYIHPQNNISCTCTCHGTYLYNDGCPGPGQDTDCPECSGFTASENHLPCHL 100  
 QY 61 SCSPCKEMGQVEISSCTVDPTVCGCRKQYHYWSENLPQCFNCSLCLNGTVHLSQOE 120  
 DB 101 SCSPCKEMGQVEISSCTVDPTVCGCRKQYHYWSENLPQCFNCSLCLNGTVHLSQOE 160  
 QY 121 KQNTVCTCHAGFFLPENECVSCNCKSLECTKLCLEPQIEN 161  
 DB 161 KQNTVCTCHAGFFLPENECVSCNCKSLECTKLCLEPQIEN 201

RESULT 8  
 AAR70108  
 ID AAR70108 standard; Protein; 309 AA  
 AC AAR70108;  
 DT 10 NOV 1995 (first entry)  
 DE TNF-R GRP fusion protein.  
 KW Hybrid peptide; malaria parasite; Plasmodium falciparum; fusion protein;  
 KW red blood cell; cytokine receptor; glycoprotein binding peptide 130;  
 KW GRP 130; GRP; glycoprotein binding peptide homologue; glycoprotein A;  
 KW tumour necrosis factor receptor; TNF-R.  
 OS Chimeric Homo sapiens.  
 OS Chimeric Plasmodium falciparum.  
 FH Key Location/Qualifiers  
 FT Misc difference 230 269  
 FT /label= repeat\_region  
 FT /note= "can be repeated n times, where n is a real  
 number"  
 XX W09506737-A.  
 XX 09 MAR 1995.  
 XX 01 SEP 1994; 94WO-GB01900.  
 XX 03 SEP 1994; 91GB-0018150  
 XX 23 AUG 1994; 94GB-0017021.  
 XX (PREN/) PRENDERCAST K F.  
 XX Prendercast KF;

XX WPI; 1995-115452/15.  
 XX New hybrid peptide(s) for binding cytokine(s) - comprising a  
 PT malaria parasite peptide capable of binding a red blood cell and  
 FT a receptor peptide.  
 XX Example A; Page 54-55; 93pp; English.  
 XX Hybrid peptides for binding cytokines, comprising a malaria parasite  
 CC (Plasmodium falciparum) peptide (capable of binding to a red blood  
 CC cell (RBC)) and a receptor peptide are claimed. AAR70108 is an example  
 CC of these hybrid peptides. AAR70108 is a fusion of tumour necrosis factor  
 CC receptor (in accordance with H. Loetscher et al. Cell, Vol. 61, 161-169)  
 CC and glycoprotein binding protein (GPB) homologue (GRP). The  
 CC use of cytokine receptors not normally found on RBCs means that the  
 CC cytokine can bind harmlessly to the RBC without deleterious effect.  
 CC The RBC protects the hybrid peptides from excretion from the kidney, and  
 CC due to steric hindrance prevents the cytokines binding to a receptor in  
 CC another cell. GRP 130 or GRP are the pref. malaria parasite peptides  
 CC used, others include EBA 175 (175 kDa erythrocyte binding antigen),  
 CC PMSA (pre major merozoite surface antigen) and the puffy binding  
 CC receptor molecule (eg. exhibited by Plasmodium vivax). These peptides  
 CC bind to pref. glycoprotein A, B and C, sialo glycoproteins, found on the  
 CC surface of RBCs. The hybrid peptides are thus used to lower the levels of  
 CC free cytokines in the circulation to reduce pathological damage.

SQ Sequence 309 AA;  
 Query Match 100.0%; Score 941; DB 16; Length 309;  
 Best Local Similarity 100.0%; Pred. No. 4.4e-67;  
 Matches 161, Conservative 0, Mismatches 0, Indels 0, Gaps 0;  
 QY 1 DSVCPQGYIHPQNNISCTCTCHGTYLYNDGCPGPGQDTDCPECSGFTASENHLPCHL 60  
 DB 20 DSVCPQGYIHPQNNISCTCTCHGTYLYNDGCPGPGQDTDCPECSGFTASENHLPCHL 79  
 QY 61 SCSPCKEMGQVEISSCTVDPTVCGCRKQYHYWSENLPQCFNCSLCLNGTVHLSQOE 120  
 DB 80 SCSPCKEMGQVEISSCTVDPTVCGCRKQYHYWSENLPQCFNCSLCLNGTVHLSQOE 139  
 QY 121 KQNTVCTCHAGFFLPENECVSCNCKSLECTKLCLEPQIEN 161  
 DB 140 KQNTVCTCHAGFFLPENECVSCNCKSLECTKLCLEPQIEN 180

RESULT 9  
 AAR89229  
 ID AAR89229 standard; Protein; 311 AA.  
 AC AAR89229;  
 DT 04-MAR-1999 (first entry)  
 DE Tumour necrosis factor bp/osteoprotegerin construct TNFbp/304.  
 XX Tumour necrosis factor receptor 1, TNF-R, inhibitor; osteoprotegerin;  
 KW OPG; chimeric; fusion; dimerisation domain; autoimmune disease;  
 KW inflammation; apoptosis.  
 OS Homo sapiens.  
 OS Synthetic.  
 XX W09849305-A1.  
 XX 05-NOV-1998.  
 XX 29-APR-1998; 98WO-US08631.  
 XX 01-MAY-1997; 97US-0850188.  
 XX (AMGE-) AMGEN INC.

[illegible]

XX	WP1: 1997-425036/39.		
XX	N FSDb; AAT94022.		
PT	Hybrid dimeric protein comprising two co-expressed units - each based on receptor or ligand and a subunit of a heterodimeric hormone, especially FSH, for inducing follicular maturation		
XX	Example; Pages 39-40; 60pp; English.		
CC	A novel fusion protein comprises 2 dimer forming co-expressed amino acid sequences, each consisting of a homodimeric or heterodimeric receptor chain or ligand, with ligand-receptor binding activity, bound directly or via a peptide linker to a subunit of a heterodimeric protein hormone capable of forming a heterodimer with the hormone's other subunits. The fusion protein, e.g. the thirubopoietin (TPO)/human chorionic gonadotrophin-beta subunit (hCG-beta) fusion protein denoted by the present sequence, significantly increases the biological activity of the hormone component, reducing the requirement for hormone itself and the number of injections needed.		
XX	Sequence 336 AA;		
XX	Query Match 100.0%; Score 941; DB 18; Length 336;		
XX	Best Local Similarity 100.0%; Fed. No. 470-67;		
XX	Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps		
QY	1 DSCGPGKTHFQNNISCTCKGKGYLVNDCGPGADDTCEKEECSFTASENHLPHCL 60		
DB	23 DSCGPGKTHFQNNISCTCKGKGYLVNDCGPGADDTCEKEECSFTASENHLPHCL 82		
QY	61 SCSCRKRENGQVEISSCTVDNDITVCGCRKNQVRYHVSNTLFCQFNCSLCLNGTVHLSQGE 120		
DB	83 SCSCRKRENGQVEISSCTVDNDITVCGCRKNQVRYHVSNTLFCQFNCSLCLNGTVHLSQGE 140		
QY	141 EGVTVCSHAGFELRENGVSSNGRSLSECTVCLHQLQEN 161		
DB	143 EGVTVCSHAGFELRENGVSSNGRSLSECTVCLHQLQEN 183		
XX	RESULT 11		
XX	AAW89228		
XX	AAW89228 standard; Protein; 366 AA.		
XX	AAW89228;		
XX	04-MAR-1999 (first entry)		
DE	Tumour necrosis factor b/ostreoprotegerin construct TNBP/248.		
XX	Tumour necrosis factor receptor 1; TNFR-1; inhibitor; osteoprotegerin		
KM	OPG; chimeric; fusion; dimerisation domain; autoimmune disease;		
XX	Inflammation; apoptosis.		
XX	Homo sapiens.		
XX	Synthetic.		
EN	W09849305-A1.		
XX	05-NOV-1998.		
XX	29-APR-1998; 98WO-US08631.		
XX	01-MAY-1997; 97US-0850188.		
FA	(AMGE-) AMGEN INC.		
XX	Boyle MJ, Wooden S;		
XX	WT1, 1999 0346C/03.		
XX	New chimeric osteoprotegerin polypeptides - contain the		

PT osteoprotegerin dimerisation domain and a heterologous sequence,  
PT useful to treat TNF and TNFR mediated disorders

XX Example 1; Fig 4; 92pp; English.

XX The present invention describes a chimeric polypeptide (A1), comprising  
XX an osteoprotegerin (OPG) dimerisation domain fused to a heterologous  
XX amino acid sequence. Also described are: (1) a multimer polypeptide  
XX comprising covalently associated A1 monomers; (2) an isolated nucleic  
XX acid encoding A1; (3) an expression vector comprising the nucleic acid  
XX sequence; and (4) a host cell transformed or transfected with the  
XX expression vector so that the nucleic acid is expressible. The products  
XX from the present invention are useful to treat a variety of disorders  
XX including those related to receptor binding. Compositions comprising  
XX tumour necrosis factor (TNF)/OPG and TNF receptor (TNFR)/OPG chimeras  
XX are used to treat TNF and TNFR-mediated disorders such as inflammation,  
XX autoimmune diseases and disorders related to excessive apoptosis. The  
XX chimeras are also useful for detecting molecules which interact with  
XX fused heterologous sequences to identify potential new receptors and  
XX ligands. The present sequence represents a TNFbp/OPG construct from  
XX the example of the present invention for creating TNFbp/OPG fusion  
XX proteins.

XX Sequence 366 AA;

Query Match 100.0%; Score 941; DB 20; Length 366;  
Best Local Similarity 100.0%; Pred. No. 5, 1e-67;  
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSVCPQCKYIHPQNNISLCTCKHKTLYLNDPCPGQDTDCRECSGFTASENHLRHCL 60  
DB 41 DSVCPQCKYIHPQNNISLCTCKHKTLYLNDPCPGQDTDCRECSGFTASENHLRHCL 100  
QY 61 SCSCKCPKEMQGVFISSCTVDPDTVCGPKNYRHYWSENLFQCFNCSLCLNGTVHLSQCE 120  
DB 101 SCSCKCPKEMQGVFISSCTVDPDTVCGPKNYRHYWSENLFQCFNCSLCLNGTVHLSQCE 160  
QY 121 KONTVCTCHAGFFPERFVSCNCFYSLEPTCLCLPQIEN 161  
DB 161 KONTVCTCHAGFFPERFVSCNCFYSLEPTCLCLPQIEN 201

RESULT 12

AAR07449  
ID AAR07449 standard; protein; 371 AA.

XX AAR07449;  
XX  
XX 29 JAN-1991 (first entry)  
XX Tumour Necrosis Factor-Binding Protein from pTNF-BP15 cDNA.

XX Tumour necrosis factor binding protein; TNF-BP; TNF-receptor;  
KW pTNF BP15; infectious disease; parasitic disease; cachexia;  
KW autoimmune disease; shock.

XX Homo sapiens.

XX EP303438 A.

XX 24 OCT 1990.

XX 06-APR 1990; 90EP-0106624.

XX 21 JUN-1989; 89DE 3920282.

XX 21 APR 1989; 89DE 3913101.

XX (BOEH ) ROEHRINGER INGELHEIMINT.

XX Hauptmann R, Himmler A, Maurer-Pogoy I, Stratowa C;

XX WPI; 1990-321987/43.

XX N-PSNR; AAQ06282.

XX DNA encoding TNF binding protein and TNF receptor used in  
PT tumour treatment and to understand mechanism to TNF action

XX Disclosure; Fig 1(1-3); 51pp; German.

XX Clone pTNF-BP15 was used to construct pADTNF-BP, for transfection of  
CC e.g. COS7 cells. The expressed proteins are useful  
CC prophylactically and therapeutically to control disorders which  
CC involve the damaging effects of TNF-alpha or -beta (e.g. infectious or  
CC parasitic diseases, shock, cachexia, autoimmune diseases, adult  
CC respiratory distress syndrome etc.), or side effects of treatment with  
CC TNF-alpha). They can also be used as diagnostic reagents for  
CC assaying TNF and in study of TNF-receptor interactions.  
XX See also AAQ06282-Q06285.

XX Sequence 371 AA;

Query Match 100.0%; Score 941; DB 11; Length 371;  
Best Local Similarity 100.0%; Pred. No. 5, 2e-67;  
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSVCPQCKYIHPQNNISLCTCKHKTLYLNDPCPGQDTDCRECSGFTASENHLRHCL 60  
DB 41 DSVCPQCKYIHPQNNISLCTCKHKTLYLNDPCPGQDTDCRECSGFTASENHLRHCL 100  
QY 61 SCSCKCPKEMQGVFISSCTVDPDTVCGPKNYRHYWSENLFQCFNCSLCLNGTVHLSQCE 120  
DB 101 SCSCKCPKEMQGVFISSCTVDPDTVCGPKNYRHYWSENLFQCFNCSLCLNGTVHLSQCE 160  
QY 121 KONTVCTCHAGFFPERFVSCNCFYSLEPTCLCLPQIEN 161  
DB 161 KONTVCTCHAGFFPERFVSCNCFYSLEPTCLCLPQIEN 201

RESULT 13

AAW89227

ID AAW89227 standard; Protein, 297 AA.

XX AAW89227;

XX 04-MAR-1999 (first entry)

XX Tumour necrosis factor bp/osteoprotegerin construct TNFbp/217.

XX Tumour necrosis factor receptor 1; TNFR-1; inhibitor; osteoprotegerin;  
KW OPG; chimeric; fusion; dimerisation domain; autoimmune disease;  
KW inflammation; apoptosis.

XX Homo sapiens.

XX Synthetic.

XX WO9849305-A1.

XX 05-NOV-1998.

XX 29-APR-1998; 98WO-US08631.

XX 01-MAY-1997; 97US-0850188.

XX (AMGE-) AMGEN INC.

XX Boyle WJ, Wooden S;

XX WPI; 1999-034661/03.

XX New chimeric osteoprotegerin polypeptides - contain the  
PT osteoprotegerin dimerisation domain and a heterologous sequence,  
PT useful to treat TNF and TNFR-mediated disorders

XX Example 1; Fig 4; 92pp; English.

XX The present invention describes a chimeric polypeptide (A1), comprising

an osteoprotegerin (OPG) dimerisation domain fused to a heterologous amino acid sequence. Also described are: (1) a multimer polypeptide comprising covalently associated A1 monomers; (2) an isolated nucleic acid encoding A1; (3) an expression vector comprising the nucleic acid sequence; and (4) a host cell transformed or transfected with the expression vector so that the nucleic acid is expressible. The products from the present invention are useful to treat a variety of disorders including those related to receptor binding. Compositions comprising tumour necrosis factor (TNF)/OPG and TNF receptor (TNFR)/OPG chimeras are used to treat TNF and TNFR-mediated disorders such as inflammation, autoimmune diseases and disorders related to excessive apoptosis. The chimeras are also useful for detecting molecules which interact with fused heterologous sequences to identify potential new receptors and ligands. The present sequence represents a TNFp/OPG construct from the example of the present invention for creating TNFp/OPG fusion proteins.

Sequence 397 AA;

Query Match 100.0%, Score 341, DB 20, Length 397;  
Best Local Similarity 100.0%, Pred. No. 5, 6e-67,  
Matches 161, Conservative 0, Mismatches 0, Indels 0, Gaps 0,

1 DSVCPGKGIHPQNNSTICTCKRKGYTLVNDGPGQDDDCRCESGSTASENHLRHCL 60  
41 DSVCPGKGIHPQNNSTICTCKRKGYTLVNDGPGQDDDCRCESGSTASENHLRHCL 100

61 SCSKCRKEMQVEISSCTVDRTVQGRKNQYHYWSENLFCQFNLSLCLNCTVHLSQCE 120  
101 SCSKCRKEMQVEISSCTVDRTVQGRKNQYHYWSENLFCQFNLSLCLNCTVHLSQCE 160

121 KQNTVCTCHAGFFLRNEVCVSCNCKKSLCTKLCIPQEN 161

161 KQNTVCTCHAGFFLRNEVCVSCNCKKSLCTKLCIPQEN 201

RESULT 14  
AAW89226  
ID AAW89226 standard; Protein: 417 AA.

AAW89226;

04 MAR-1999 (first entry)

Tumour necrosis factor lg/osteoprotegerin construct TNFp/196.

Tumour necrosis factor receptor 1, TNFR 1, inhibitor, osteoprotegerin;  
OPG, chimeric, fusion, dimerisation domain, autoimmune disease;  
inflammation; apoptosis.

Homo sapiens.

Synthetic.

W09849305-A1.

05 NOV-1998.

29 APR-1998; 98WO-US08631.

01 MAY-1997; 97US-0850188.

(AMGE-) AMGEN INC.

Boyle WJ, Wooden S;

WPI; 1999-034661/03.

New chimeric osteoprotegerin polypeptides - contain the  
osteoprotegerin dimerisation domain and a heterologous sequence,  
useful to treat TNF and TNFR mediated disorders

Example 1; Fig 4; 92pp; English.

The present invention describes a chimeric polypeptide (A1), comprising an osteoprotegerin (OPG) dimerisation domain fused to a heterologous amino acid sequence. Also described are: (1) a multimer polypeptide comprising covalently associated A1 monomers; (2) an isolated nucleic acid encoding A1; (3) an expression vector comprising the nucleic acid sequence; and (4) a host cell transformed or transfected with the expression vector so that the nucleic acid is expressible. The products from the present invention are useful to treat a variety of disorders including those related to receptor binding. Compositions comprising tumour necrosis factor (TNF)/OPG and TNF receptor (TNFR)/OPG chimeras are used to treat TNF and TNFR-mediated disorders such as inflammation, autoimmune diseases and disorders related to excessive apoptosis. The chimeras are also useful for detecting molecules which interact with fused heterologous sequences to identify potential new receptors and ligands. The present sequence represents a TNFp/OPG construct from the example of the present invention for creating TNFp/OPG fusion proteins.

Sequence 417 AA;

Query Match 100.0%, Score 341; DB 20, Length 417;  
Best Local Similarity 100.0%, Pred. No. 5, 8e-67,  
Matches 161, Conservative 0, Mismatches 0, Indels 0, Gaps 0;

1 DSVCPGKGIHPQNNSTICTCKRKGYTLVNDGPGQDDDCRCESGSTASENHLRHCL 60  
41 DSVCPGKGIHPQNNSTICTCKRKGYTLVNDGPGQDDDCRCESGSTASENHLRHCL 100

61 SCSKCRKEMQVEISSCTVDRTVQGRKNQYHYWSENLFCQFNLSLCLNCTVHLSQCE 120  
101 SCSKCRKEMQVEISSCTVDRTVQGRKNQYHYWSENLFCQFNLSLCLNCTVHLSQCE 160

121 KQNTVCTCHAGFFLRNEVCVSCNCKKSLCTKLCIPQEN 161

161 KQNTVCTCHAGFFLRNEVCVSCNCKKSLCTKLCIPQEN 201

RESULT 15  
AAW89224  
ID AAW89224 standard; Protein: 420 AA.

AAW89224;

04 MAR-1999 (first entry)

Tumour necrosis factor bp/osteoprotegerin construct TNFp/OPG.

Tumour necrosis factor receptor 1, TNFR 1, inhibitor, osteoprotegerin;  
OPG, chimeric, fusion, dimerisation domain, autoimmune disease;  
inflammation; apoptosis.

Homo sapiens.

Synthetic.

W09849305-A1.

05 NOV-1998.

29 APR-1998; 98WO-US08631.

01 MAY-1997; 97US-0850188.

(AMGE-) AMGEN INC.

Boyle WJ, Wooden S;

WPI; 1999-034661/03.

New chimeric osteoprotegerin polypeptides - contain the  
osteoprotegerin dimerisation domain and a heterologous sequence,  
useful to treat TNF and TNFR mediated disorders

Example 1; Fig 4; 92pp; English.

XX The present invention describes a chimeric polypeptide (A1), comprising  
 CC an osteoprotegerin (OPG) dimerisation domain fused to a heterologous  
 CC amino acid sequence. Also described are: (1) a multimer polypeptide  
 CC comprising covalently associated A1 monomers; (2) an isolated nucleic  
 CC acid encoding A1; (3) an expression vector comprising the nucleic acid  
 CC sequence; and (4) a host cell transformed or transfected with the  
 CC expression vector so that the nucleic acid is expressible. The products  
 CC from the present invention are useful to treat a variety of disorders  
 CC including those related to receptor binding. Compositions comprising  
 CC tumour necrosis factor (TNF)/OPG and TNF receptor (TNFR)/OPG chimeras  
 CC are used to treat TNF and TNFR-mediated disorders such as inflammation,  
 CC autoimmune diseases and disorders related to excessive apoptosis. The  
 CC chimeras are also useful for detecting molecules which interact with  
 CC fused heterologous sequences to identify potential new receptors and  
 CC ligands. The present sequence represents a TNFbp/OPG construct from  
 CC the example of the present invention for creating TNFbp/OPG fusion  
 CC proteins.

XX SQ Sequence 420 AA;

Query Match	100.0%	Score 941;	DB 20;	Length 420;
Best Local Similarity	100.0%	Pred. No. 5.8e-67;		
Matches 161;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	1	DSVCPQGRVYHPQNNISICTKHKTLYLNDPCPGQDTDCPECSGFTASENHLPHCL	60
DB	41	DSVCPQGRVYHPQNNISICTKHKTLYLNDPCPGQDTDCPECSGFTASENHLPHCL	100
QY	61	SSSKPRKMGQVEISSCTVDGNTVCGPKNQYPHYWSENLFQCFNCSLCLNGTVHLSQCE	120
DB	101	SSSKPRKMGQVEISSCTVDGNTVCGPKNQYPHYWSENLFQCFNCSLCLNGTVHLSQCE	160
QY	121	KONTVCTCHAGFFLRNEKVCSCNCKSLECTKLCLPOIEN	161
DB	161	KONTVCTCHAGFFLRNEKVCSCNCKSLECTKLCLPOIEN	201

Search completed: January 6, 2003, 03:57:45  
 Job time : 41 secs



GenCore version 5.1.3  
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OM protein protein search, using sw model

Run on: January 6, 2003, 03:57:07 / Search time 17 Seconds  
(without alignments)  
278.652 Million cell updates/sec

Title: US-09-882-735-2

Perfect score: 941

Sequence: 1 DSVCPQGYIHQNNISICT ..... CSNCKYSRECTVLCPLQIEN 161

Scoring table: BLOSUM62

Gapop 10 0 , Gapext 0 5

Searched: 262574 seqs, 2942922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.\*

1: /cqn2\_6/prodata/1/iaa/5A.COMB.pep.\*

2: /cqn2\_6/prodata/1/iaa/6A.COMB.pep.\*

3: /cqn2\_6/prodata/1/iaa/6A.COMB.pep.\*

4: /cqn2\_6/prodata/1/iaa/6A.COMB.pep.\*

5: /cqn2\_6/prodata/1/iaa/6A.COMB.pep.\*

6: /cqn2\_6/prodata/1/iaa/6A.COMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	941	100.0	161	US 09 326-394 2	Sequence 2, Appl
2	941	100.0	280	US 08-974 022-46	Sequence 46, Appl
3	941	100.0	280	US 08-795-445A-46	Sequence 46, Appl
4	941	100.0	280	US 08-795-447A-46	Sequence 46, Appl
5	941	100.0	280	US 08-974-186-46	Sequence 46, Appl
6	941	100.0	280	US 08-795-446B-46	Sequence 46, Appl
7	941	100.0	280	US 08-706 945D-132	Sequence 132, Appl
8	941	100.0	336	US 08-804-166-8	Sequence 8, Appl
9	941	100.0	336	US 08-910-991-8	Sequence 8, Appl
10	941	100.0	455	US 08-050 319B-25	Sequence 25, Appl
11	941	100.0	455	US 08-321 668-2	Sequence 2, Appl
12	941	100.0	455	US 08-837-941-2	Sequence 2, Appl
13	941	100.0	455	US 08-126-016-2	Sequence 2, Appl
14	941	100.0	455	US 08-465-982-25	Sequence 25, Appl
15	941	100.0	455	US 08-815-469-5	Sequence 5, Appl
16	941	100.0	455	US 09-006-353A-3	Sequence 3, Appl
17	941	100.0	455	US 08-527-236A 5	Sequence 5, Appl
18	941	100.0	455	US 08-054-970-2	Sequence 2, Appl
19	941	100.0	455	US 08-565-918-4	Sequence 4, Appl
20	941	100.0	455	US 09-573-986-3	Sequence 3, Appl
21	930.5	98.9	909	US 09-013-895A-4	Sequence 4, Appl
22	930.5	98.9	909	US 09-448-868-4	Sequence 4, Appl
23	928	98.6	285	US 08-804-166-6	Sequence 6, Appl
24	928	98.6	285	US 08-910-991-6	Sequence 6, Appl
25	925.5	98.4	453	US 08-086-483A-5	Sequence 5, Appl
26	924	98.2	199	US 08-050-319B-48	Sequence 48, Appl
27	924	98.2	199	US 08-465-982 48	Sequence 48, Appl

28	921	97.9	197	4	US-08-828-683A-21	Sequence 21, Appl
29	904	96.1	154	4	US 08 828 683A-12	Sequence 12, Appl
30	900	95.6	152	2	US 08 219 237B 4	Sequence 4, Appl
31	900	95.6	153	4	US-08-477-347-12	Sequence 12, Appl
32	900	95.6	153	4	US-08-476-862-3	Sequence 4, Appl
33	900	95.6	153	4	US-08-468-560C-4	Sequence 4, Appl
34	873	92.8	154	2	US-08-232-087A 10	Sequence 10, Appl
35	842.5	89.5	256	4	US 08 804 166 2	Sequence 2, Appl
36	842.5	89.5	256	4	US 08 910 991 2	Sequence 2, Appl
37	837	88.9	307	4	US-08-804-166-4	Sequence 4, Appl
38	837	88.9	307	4	US-08-910-991-4	Sequence 4, Appl
39	822	87.4	139	4	US-08 706 945D 129	Sequence 129, Appl
40	746	79.3	167	1	US-08-050 319B-2	Sequence 2, Appl
41	746	79.3	167	1	US 08 050 319B-57	Sequence 57, Appl
42	746	79.3	167	2	US-08-465-982 2	Sequence 2, Appl
43	746	79.3	167	2	US 08 465 982-57	Sequence 57, Appl
44	731	77.7	124	1	US-08-050 319B-4	Sequence 4, Appl
45	731	77.7	124	2	US-08-465-982-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1  
US-09-326-394-2  
; Sequence 2, Application US/09326394  
; Patent No. 6306820  
; GENERAL INFORMATION:  
; APPLICANT: Bendele, Alison M.  
; APPLICANT: Sennello, Regina M.  
; TITLE OF INVENTION: COMBINATION THERAPY USING A TGF BINDING  
; TITLE OF INVENTION: PROTEIN FOR TREATING TNF-MEDIATED DISEASES  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Amgen Inc.  
; STREET: 1840 DeHavilland Drive  
; CITY: Thousand Oaks  
; STATE: CA  
; COUNTRY: US  
; ZIP: 91320-1789  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/326,394  
; FILING DATE: 08-DEC-1997  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/032,587  
; FILING DATE: 06 DEC 1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/036,355  
; FILING DATE: 23-JAN-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/039,315  
; FILING DATE: 07 FEB 1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/052,023  
; FILING DATE: 09-JUL-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Zindrick, Thomas K.  
; REGISTRATION NUMBER: 32,185  
; REFERENCE/DOCKET NUMBER: A-430D  
; INFORMATION FOR SEQ ID NO. 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 161 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-326-394-2

Query Match 100.0%, Score 941, DB 4, Length 161;  
Best Local Similarity 100.0%; Pred. No. 1.6e-76;  
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

UY 1 DSVCPGQKVIHPNNSICTKCHKGTLYNDGPGQDDDCRECEGSGFTASENHLRHCL 60  
DB 1 DSVCPGQKVIHPNNSICTKCHKGTLYNDGPGQDDDCRECEGSGFTASENHLRHCL 60  
UY 61 SCSKREKMGVEISSCTVDRDTCGGRKQYRHYWSENLFQCFNCSCLNGTVHLSQCE 120  
DB 61 SCSKREKMGVEISSCTVDRDTCGGRKQYRHYWSENLFQCFNCSCLNGTVHLSQCE 120  
UY 121 KONTVCTCHAGFFLENECVSCNCKKSLCTKLCPLQIEN 161  
DB 121 KONTVCTCHAGFFLENECVSCNCKKSLCTKLCPLQIEN 161

## RESULT 2

US-08-974-022-46  
Sequence 46, Application US/08974022  
Patent No. 6015938  
GENERAL INFORMATION:  
APPLICANT: Boyle, William J.  
APPLICANT: Lacey, David L.  
APPLICANT: Calzone, Frank J.  
APPLICANT: Chang, Ming-Shi  
TITLE OF INVENTION: OSTEOPROTEGERIN  
NUMBER OF SEQUENCES: 53  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Amgen Inc.  
STREET: 1840 Dehavilland Drive  
CITY: Thousand Oaks  
STATE: California  
COUNTRY: USA  
ZIP: 91320-1789  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/974,022  
FILING DATE: 12-DEC-1995  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/577,788  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Wintner, Robert B.  
REFERENCE/DOCKET NUMBER: A-378  
INFORMATION FOR SEQ ID NO: 46:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 280 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-974-022 46

Query Match 100.0%; Score 941; DB 3; Length 280;  
Best Local Similarity 100.0%; Pred. No. 2.7e-76;  
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

UY 1 DSVCPGQKVIHPNNSICTKCHKGTLYNDGPGQDDDCRECEGSGFTASENHLRHCL 60  
DB 41 DSVCPGQKVIHPNNSICTKCHKGTLYNDGPGQDDDCRECEGSGFTASENHLRHCL 100  
UY 61 SCSKREKMGVEISSCTVDRDTCGGRKQYRHYWSENLFQCFNCSCLNGTVHLSQCE 120  
DB 101 SCSKREKMGVEISSCTVDRDTCGGRKQYRHYWSENLFQCFNCSCLNGTVHLSQCE 160  
UY 121 KONTVCTCHAGFFLENECVSCNCKKSLCTKLCPLQIEN 161

DB 161 KONTVCTCHAGFFLENECVSCNCKKSLCTKLCPLQIEN 201

## RESULT 3

US-08-795-445A-46  
Sequence 46, Application US/08795445A  
Patent No. 6284485  
GENERAL INFORMATION:  
APPLICANT: Boyle, William J.  
APPLICANT: Lacey, David L.  
APPLICANT: Calzone, Frank J.  
APPLICANT: Chang, Ming-Shi  
TITLE OF INVENTION: OSTEOPROTEGERIN  
NUMBER OF SEQUENCES: 53  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Amgen Inc.  
STREET: 1840 Dehavilland Drive  
CITY: Thousand Oaks  
STATE: California  
COUNTRY: USA  
ZIP: 91320-1789  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/795,445A  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/577,788  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Wintner, Robert B.  
REFERENCE/DOCKET NUMBER: A-378  
INFORMATION FOR SEQ ID NO: 46:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 280 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-795-445A-46

Query Match 100.0%; Score 941; DB 4; Length 280;  
Best Local Similarity 100.0%; Pred. No. 2.7e-76;  
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

UY 1 DSVCPGQKVIHPNNSICTKCHKGTLYNDGPGQDDDCRECEGSGFTASENHLRHCL 60  
DB 41 DSVCPGQKVIHPNNSICTKCHKGTLYNDGPGQDDDCRECEGSGFTASENHLRHCL 100  
UY 61 SCSKREKMGVEISSCTVDRDTCGGRKQYRHYWSENLFQCFNCSCLNGTVHLSQCE 120  
DB 101 SCSKREKMGVEISSCTVDRDTCGGRKQYRHYWSENLFQCFNCSCLNGTVHLSQCE 160  
UY 121 KONTVCTCHAGFFLENECVSCNCKKSLCTKLCPLQIEN 161  
DB 161 KONTVCTCHAGFFLENECVSCNCKKSLCTKLCPLQIEN 201

## RESULT 4

US-08-795-447A-46  
Sequence 46, Application US/08795447A  
Patent No. 6284728  
GENERAL INFORMATION:  
APPLICANT: Boyle, William J.  
APPLICANT: Lacey, David L.  
APPLICANT: Calzone, Frank J.  
APPLICANT: Chang, Ming-Shi  
TITLE OF INVENTION: Osteoprotegerin



```

; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: One Amgen Center Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/795,447A
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-37402
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 280 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-795-447A 46

Query Match 100.0%; Score 941; DB 4; Length 280;
Best Local Similarity 100.0%; Pred. No. 2.7e-76;
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSVCPQGYIHPQNNISICTKHKGTLYNCPGPGQDTDCPECESGSFTASENHLPHCL 60
DB 41 DSVCPQGYIHPQNNISICTKHKGTLYNCPGPGQDTDCPECESGSFTASENHLPHCL 100
QY 61 SCSKCPKEMGQVEISSCTVDPTVCGCPKQYHYWSENLPQCFNCSCLNGTVHLSQCE 120
DB 101 SCSKCPKEMGQVEISSCTVDPTVCGCPKQYHYWSENLPQCFNCSCLNGTVHLSQCE 160
QY 121 KONTVCTCHAGFLPENECVSCNCKKSLCTKLCLPQIEN 161
DB 161 KONTVCTCHAGFLPENECVSCNCKKSLCTKLCLPQIEN 201

RESULT 5
US 08 974 186-46
; Sequence 46, Application US/08974186
; Patent No. 6,284,740
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; APPLICANT: Lacey, David L.
; APPLICANT: Calzone, Frank J.
; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: OSTEOPROTEGERIN
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 Dehavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,186
; FILING DATE:
; CLASSIFICATION:

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/577,788
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-378
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 280 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-974-186-46

Query Match 100.0%; Score 941; DB 4; Length 280;
Best Local Similarity 100.0%; Pred. No. 2.7e-76;
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSVCPQGYIHPQNNISICTKHKGTLYNCPGPGQDTDCPECESGSFTASENHLPHCL 60
DB 41 DSVCPQGYIHPQNNISICTKHKGTLYNCPGPGQDTDCPECESGSFTASENHLPHCL 100
QY 61 SCSKCPKEMGQVEISSCTVDPTVCGCPKQYHYWSENLPQCFNCSCLNGTVHLSQCE 120
DB 101 SCSKCPKEMGQVEISSCTVDPTVCGCPKQYHYWSENLPQCFNCSCLNGTVHLSQCE 160
QY 121 KONTVCTCHAGFLPENECVSCNCKKSLCTKLCLPQIEN 161
DB 161 KONTVCTCHAGFLPENECVSCNCKKSLCTKLCLPQIEN 201

RESULT 6
US-08-795-446B-46
; Sequence 46, Application US/08795446B
; Patent No. 628032
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; APPLICANT: Lacey, David L.
; APPLICANT: Calzone, Frank J.
; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: OSTEOPROTEGERIN
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 Dehavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.40
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/795,446B
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/577,788
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-378
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 280 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-795-446B-46

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Query Match 100.0%, Score 941, DB 4, Length 280;  
Best Local Similarity 100.0%, Pred No. 2 7e-76;  
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSVCPQGYIHPQNNISICTKCHKGTLYNDGPGQDTCRCESGSPFASENHLRHCL 60  
DB 41 DSVCPQGYIHPQNNISICTKCHKGTLYNDGPGQDTCRCESGSPFASENHLRHCL 100  
CY 4 SCSCRKEMQGVLEISCTVDRTVCGGRKQYRHWSENLFQCFNCSLCLNGTVHLSQCE 120  
DB 101 SCSCRKEMQGVLEISCTVDRTVCGGRKQYRHWSENLFQCFNCSLCLNGTVHLSQCE 160  
CY 121 KNTVCTCHAGFLFLENFECVSCSNCKSKSECTKLCPLQIEN 161  
DB 161 KNTVCTCHAGFLFLENFECVSCSNCKSKSECTKLCPLQIEN 201

RESULT 7  
US-08-706-945D-132  
Sequence 132, Application US/970645D  
Patent No. 6369027  
GENERAL INFORMATION:  
APPLICANT: Boyte, William  
APPLICANT: Lacey, David  
APPLICANT: Calzone, Frank  
APPLICANT: Chang, Ming-Shi  
TITLE OF INVENTION: Osteoprotegerin  
FILE REFERENCE: A-378CIP  
CURRENT APPLICATION NUMBER: US/08/706,945D  
CURRENT FILING DATE: 1996-09-03  
PRIORITY FILING DATE: 1995-12-22  
PRIORITY FILING DATE: 1995-12-22  
NUMBER OF SEQ ID NOS: 145  
SOFTWARE: Patent in version 3.1  
SEQ ID NO 132  
LENGTH: 280  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-08-706-945D-132

Query Match 100.0%, Score 941, DB 4, Length 280;  
Best Local Similarity 100.0%, Pred No. 2 7e-76;  
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSVCPQGYIHPQNNISICTKCHKGTLYNDGPGQDTCRCESGSPFASENHLRHCL 60  
DB 41 DSVCPQGYIHPQNNISICTKCHKGTLYNDGPGQDTCRCESGSPFASENHLRHCL 100  
CY 4 SCSCRKEMQGVLEISCTVDRTVCGGRKQYRHWSENLFQCFNCSLCLNGTVHLSQCE 120  
DB 101 SCSCRKEMQGVLEISCTVDRTVCGGRKQYRHWSENLFQCFNCSLCLNGTVHLSQCE 160  
CY 121 KNTVCTCHAGFLFLENFECVSCSNCKSKSECTKLCPLQIEN 161  
DB 161 KNTVCTCHAGFLFLENFECVSCSNCKSKSECTKLCPLQIEN 201

RESULT 8  
US-08-804-166-8  
Sequence 8, Application US/08804166.  
Patent No. 6193972  
GENERAL INFORMATION:  
APPLICANT: Campbell, Robert K.  
APPLICANT: Jameson, Bradford A.  
APPLICANT: Chapel, Scott C.  
TITLE OF INVENTION: HYBRID PROTEINS  
NUMBER OF SEQUENCES: 22  
CORRESPONDENCE ADDRESS:  
ADDRESS: HPOMDY AND NEIMARK  
STREET: 419 Seventh Street N.W., Ste. 300  
CITY: Washington  
STATE: D.C.

COUNTRY: USA  
ZIP: 22207  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/804,166  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/011,936  
FILING DATE: 20 February 1996  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Browdy, Roger L.  
REGISTRATION NUMBER: 25,618  
REFERENCE/DOCKET NUMBER: CAMPBELL=2A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 628-5197  
TELEFAX: (202) 737-3528  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 336 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-804-166-8

Query Match 100.0%, Score 941, DB 4, Length 336;  
Best Local Similarity 100.0%, Pred No. 3 2e-76;  
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSVCPQGYIHPQNNISICTKCHKGTLYNDGPGQDTCRCESGSPFASENHLRHCL 60  
DB 23 DSVCPQGYIHPQNNISICTKCHKGTLYNDGPGQDTCRCESGSPFASENHLRHCL 82  
QY 4 SCSCRKEMQGVLEISCTVDRTVCGGRKQYRHWSENLFQCFNCSLCLNGTVHLSQCE 120  
DB 83 SCSCRKEMQGVLEISCTVDRTVCGGRKQYRHWSENLFQCFNCSLCLNGTVHLSQCE 142  
CY 121 KNTVCTCHAGFLFLENFECVSCSNCKSKSECTKLCPLQIEN 161  
DB 143 KNTVCTCHAGFLFLENFECVSCSNCKSKSECTKLCPLQIEN 183

RESULT 9  
US-08-910-991-8  
Sequence 8, Application US/08910991  
Patent No. 6194177  
GENERAL INFORMATION:  
APPLICANT: Campbell, Robert K.  
APPLICANT: Jameson, Bradford A.  
APPLICANT: Chapel, Scott C.  
TITLE OF INVENTION: HYBRID PROTEINS  
NUMBER OF SEQUENCES: 22  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BROWDY AND NEIMARK  
STREET: 419 Seventh Street N.W., Ste. 300  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 22207  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/910,991  
FILING DATE:  
CLASSIFICATION: 530

; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/004,166  
 ; FILING DATE: 20 February 1997  
 ; PRIOR APPLICATION DATA: 60/011,936  
 ; FILING DATE: 20 February 1996  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: YUN, Allen C.  
 ; REGISTRATION NUMBER: 37,971  
 ; REFERENCE/DOCKET NUMBER: CAMPBELL-2B  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (202) 628-5197  
 ; TELEFAX: (202) 737-3528  
 ; INFORMATION FOR SEQ ID NO: 8:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 316 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US 08 910-991-8

Query Match 100.0%; Score 941; DB 4; Length 336;  
 Best Local Similarity 100.0%; Pred. No. 3.2e-76;  
 Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSVCPQCKYIHPQNNISICTYCHKTYLYNDGPGGQDTCPPEESGFTASENHLPHCL 60  
 DB 23 DSVCPQCKYIHPQNNISICTYCHKTYLYNDGPGGQDTCPPEESGFTASENHLPHCL 82  
 QY 61 SCSKPKFMQGVFISSTVDRTVCGPKNQYPHYWSENLFQCFNCSLCLNGTIVHLSQCE 120  
 DB 83 SCSKPKFMQGVFISSTVDRTVCGPKNQYPHYWSENLFQCFNCSLCLNGTIVHLSQCE 142  
 QY 121 KNTVCTCHAGFFLRENEVCSCNCKESLCTKLCLOPIEN 161  
 DB 143 KNTVCTCHAGFFLRENEVCSCNCKESLCTKLCLOPIEN 193

RESULT 10  
 US-08-050-319B-25  
 ; Sequence 25, Application US/08050319B  
 ; Patent No. 5613145  
 ; GENERAL INFORMATION:  
 ; APPLICANT: M. Feldmann, P. W. Gray.  
 ; APPLICANT: M.J.C. Turner, F.M. Brennan  
 ; TITLE OF INVENTION: Modified human TNFalpha (Tumor  
 ; TITLE OF INVENTION: Necrosis Factor alpha) Receptor  
 ; NUMBER OF SEQUENCES: 57  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Reed & Robbins  
 ; STREET: 635 Bryant Street  
 ; CITY: Palo Alto  
 ; STATE: California  
 ; COUNTRY: USA  
 ; ZIP: 94301  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/050,319B  
 ; FILING DATE: 10-May-1993  
 ; CLASSIFICATION: 435  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Robbins, Robert L.  
 ; REGISTRATION NUMBER: 33,208  
 ; REFERENCE/DOCKET NUMBER: 5150-0030  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (415) 617-8999  
 ; TELEFAX: (415) 327-3231  
 ; INFORMATION FOR SEQ ID NO: 25:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 316 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US 08 910-991-8

; LENGTH: 455 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-08-050-319B-25  
 Query Match 100.0%; Score 941; DB 1; Length 406;  
 Best Local Similarity 100.0%; Pred. No. 4.3e-76;  
 Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSVCPQCKYIHPQNNISICTYCHKTYLYNDGPGGQDTCPPEESGFTASENHLPHCL 60  
 DB 41 DSVCPQCKYIHPQNNISICTYCHKTYLYNDGPGGQDTCPPEESGFTASENHLPHCL 100  
 QY 61 SCSKPKFMQGVFISSTVDRTVCGPKNQYPHYWSENLFQCFNCSLCLNGTIVHLSQCE 120  
 DB 101 SCSKPKFMQGVFISSTVDRTVCGPKNQYPHYWSENLFQCFNCSLCLNGTIVHLSQCE 160  
 QY 121 KNTVCTCHAGFFLRENEVCSCNCKESLCTKLCLOPIEN 161  
 DB 161 KNTVCTCHAGFFLRENEVCSCNCKESLCTKLCLOPIEN 201

RESULT 11  
 US-08-321-668-2  
 ; Sequence 2, Application US/08321668  
 ; Patent No. 5665859  
 ; GENERAL INFORMATION:  
 ; APPLICANT: WALLACH, David  
 ; APPLICANT: BRAEBUSCH, Cord  
 ; APPLICANT: VARFLOMBEV, Eugene  
 ; APPLICANT: BATYIN, Michael  
 ; TITLE OF INVENTION: MOLECULES INFLUENCING THE SHEEDING OF  
 ; TITLE OF INVENTION: THE TNF RECEPTORS, THEIR PREPARATION AND THEIR USE  
 ; NUMBER OF SEQUENCES: 42  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: BROWDY AND NEIMARK  
 ; STREET: 419 Seventh Street, N.W., Suite 300  
 ; CITY: Washington  
 ; STATE: D.C.  
 ; COUNTRY: USA  
 ; ZIP: 20004  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/321,668  
 ; FILING DATE: 12-OCT-1994  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: IL 107268  
 ; FILING DATE: 12-OCT-1993  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: BROWDY, Roger L.  
 ; REGISTRATION NUMBER: 25,618  
 ; REFERENCE/DOCKET NUMBER: WALLACH-13  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 202-628-5197  
 ; TELEFAX: 202-737-3528  
 ; TELEX: 248633  
 ; INFORMATION FOR SEQ ID NO: 2:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 455 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-08-321-668-2

Query Match 100.0%; Score 941; DB 1; Length 406;  
 Best Local Similarity 100.0%; Pred. No. 4.3e-76;  
 Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



RESULT 14

US 08 465-982-25  
 : Sequence 25, Application US/08465982  
 : Patent No. 5863786  
 : GENERAL INFORMATION:  
 : APPLICANT: M. Feldmann, P.W. Gray,  
 : APPLICANT: M.J.C. Turner, F.M. Brennan  
 : TITLE OF INVENTION: Modified human TNFalpha (Tumor  
 : TITLE OF INVENTION: Necrosis Factor alpha) Receptor  
 : NUMBER OF SEQUENCES: 57  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESSEE: Read & Robbins  
 : STREET: 645 Bryant Street  
 : CITY: Palo Alto  
 : STATE: California  
 : COUNTRY: USA  
 : ZIP: 94301  
 : COMPUTER READABLE FORM:  
 : MEDIUM TYPE: Floppy disk  
 : COMPUTER: IBM PC compatible  
 : OPERATING SYSTEM: PC-DOS/MS-DOS  
 : SOFTWARE: Patent In Release #1.0, version #1.25  
 : CURRENT APPLICATION DATA:  
 : APPLICATION NUMBER: US/08/465,982  
 : FILING DATE:  
 : CLASSIFICATION:  
 : PRIOR APPLICATION DATA:  
 : APPLICATION NUMBER: US/08/050,319  
 : FILING DATE: 10-May-1993  
 : ATTORNEY/AGENT INFORMATION:  
 : NAME: Robbins, Robert L.  
 : REGISTRATION NUMBER: 33,208  
 : REFERENCE/DOCKET NUMBER: 5150-0010  
 : TELECOMMUNICATION INFORMATION:  
 : TELEPHONE: (415) 617-8999  
 : TELEFAX: (415) 327-3231  
 : INFORMATION FOR SEQ ID NO. 25:  
 : SEQUENCE CHARACTERISTICS:  
 : LENGTH: 455 amino acids  
 : TYPE: amino acid  
 : TOPOLOGY: linear  
 : MOLECULE TYPE: protein  
 : US 08 465-982-25

Query Match 100.0%; Score 941; DB 2; Length 455;

Best Local Similarity 100.0%; Pred. No. 4.3e-76;

Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSVCPQGYIHPQNNISICCTKCHKTYLYNDGPGQDTPCEGSGFTASENHLPHCL 60  
 DB 41 DSVCPQGYIHPQNNISICCTKCHKTYLYNDGPGQDTPCEGSGFTASENHLRHCL 100  
 QY 61 SCSKCPKEMGQVEISSUTVDFPTVCGGPFQYHYWSENLFQCFNCSLCLNGTVHLSQCE 120  
 DB 101 SCSKCPKEMGQVEISSUTVDFPTVCGGPFQYHYWSENLFQCFNCSLCLNGTVHLSQCE 160  
 QY 121 KONTVCTCHAGFFLPENECVSCNCKKSLCTKLCPLQIEN 161  
 DB 161 KONTVCTCHAGFFLPENECVSCNCKKSLCTKLCPLQIEN 201

RESULT 15

US 08 815-469-5  
 : Sequence 5, Application US/08815469  
 : Patent No. 6153402  
 : GENERAL INFORMATION:  
 : APPLICANT: Yu, Guo-Liang  
 : APPLICANT: Ni, Jian  
 : APPLICANT: Dixit, Vishva  
 : APPLICANT: Gentz, Reiner L.  
 : APPLICANT: Dillon, Patrick J.  
 : TITLE OF INVENTION: Death Domain Containing Receptors  
 : NUMBER OF SEQUENCES: 17

: CORRESPONDENCE ADDRESS:  
 : ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.  
 : STREET: 1100 New York Ave., NW, Suite 600  
 : CITY: Washington  
 : STATE: DC  
 : COUNTRY: USA  
 : ZIP: 20005-3934  
 : COMPUTER READABLE FORM:  
 : MEDIUM TYPE: Floppy disk  
 : COMPUTER: IBM PC compatible  
 : OPERATING SYSTEM: PC-DOS/MS-DOS  
 : SOFTWARE: Patent In Release #1.0, Version #1.10  
 : CURRENT APPLICATION DATA:  
 : APPLICATION NUMBER: US/08/815,469  
 : FILING DATE: HEREWITH  
 : CLASSIFICATION: 435  
 : PRIOR APPLICATION DATA:  
 : APPLICATION NUMBER: No. 6153402 Yet Assigned  
 : FILING DATE: 06-FEB-1997  
 : PRIOR APPLICATION DATA:  
 : APPLICATION NUMBER: US 60/028,711  
 : FILING DATE: 17-OCT-1996  
 : PRIOR APPLICATION DATA:  
 : APPLICATION NUMBER: US 60/013,285  
 : FILING DATE: 12-MAR-1996  
 : ATTORNEY/AGENT INFORMATION:  
 : NAME: Steffe, Eric K.  
 : REGISTRATION NUMBER: 36,688  
 : REFERENCE/DOCKET NUMBER: 1488.0310003/EKS/KRM  
 : TELECOMMUNICATION INFORMATION:  
 : TELEPHONE: 202-371-2600  
 : TELEFAX: 202-371-2540  
 : INFORMATION FOR SEQ ID NO. 5:  
 : SEQUENCE CHARACTERISTICS:  
 : LENGTH: 455 amino acids  
 : TYPE: amino acid  
 : STRANDEDNESS: not relevant  
 : TOPOLOGY: not relevant  
 : MOLECULE TYPE: protein  
 : US-08-815-469-5

Query Match 100.0%; Score 941; DB 4; Length 455;

Best Local Similarity 100.0%; Pred. No. 4.3e-76;

Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSVCPQGYIHPQNNISICCTKCHKTYLYNDGPGQDTPCEGSGFTASENHLPHCL 60  
 DB 41 DSVCPQGYIHPQNNISICCTKCHKTYLYNDGPGQDTPCEGSGFTASENHLRHCL 100  
 QY 61 SCSKCPKEMGQVEISSUTVDFPTVCGGPFQYHYWSENLFQCFNCSLCLNGTVHLSQCE 120  
 DB 101 SCSKCPKEMGQVEISSUTVDFPTVCGGPFQYHYWSENLFQCFNCSLCLNGTVHLSQCE 160  
 QY 121 KONTVCTCHAGFFLPENECVSCNCKKSLCTKLCPLQIEN 161  
 DB 161 KONTVCTCHAGFFLPENECVSCNCKKSLCTKLCPLQIEN 201

Search completed: January 6, 2003, 04:00:13

Job time : 27 secs





DB 61 SCSSKREMGVEIISCTVDRDTCVCGCKKQYRHWSENLFQCFNCSCLNGTVHLSQCE 120  
QY 121 KONTVCTCHAGFFLENECVSCNCKRKSLECTCTLCPOIEN 161  
DB 121 KONTVCTCHAGFFLENECVSCNCKRKSLECTCTLCPOIEN 161  
RESULT 2  
US-09-899-429A-4  
Sequence 4, Application US/09899429A  
Patent No. US2002016918A1  
GENERAL INFORMATION:  
APPLICANT: Hauptmann, Rudolph  
APPLICANT: Hummeler, Adolph  
APPLICANT: Maurer-Fogy, Ingrid  
APPLICANT: Stratowa, Christian  
TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for  
FILE REFERENCE: 98,385-J  
CURRENT FILING DATE: 2001-07-03  
PRIOR APPLICATION NUMBER: 09/792,356  
PRIOR FILING DATE: 2000-02-23  
PRIOR APPLICATION NUMBER: 06/477,539  
PRIOR FILING DATE: 1985-06-07  
PRIOR APPLICATION NUMBER: 08/383,676  
PRIOR FILING DATE: 1995-02-01  
PRIOR APPLICATION NUMBER: 08/153,287  
PRIOR FILING DATE: 1993-11-17  
PRIOR APPLICATION NUMBER: 07/821,750  
PRIOR FILING DATE: 1992-01-02  
PRIOR APPLICATION NUMBER: 07/511,430  
PRIOR FILING DATE: 1990-04-20  
NUMBER OF SEQ ID NOS: 97  
SOFTWARE: Patent In Ver. 2.0  
SEQ ID NO 4  
LENGTH: 161  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-899-429A-4  
Query Match 100.0%; Score 941; DB 9; Length 161;  
Best Local Similarity 100.0%; Pred No. 2.8e-61;  
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 121 KONTVCTCHAGFFLENECVSCNCKRKSLECTCTLCPOIEN 161  
DB 61 SCSSKREMGVEIISCTVDRDTCVCGCKKQYRHWSENLFQCFNCSCLNGTVHLSQCE 120  
QY 61 SCSSKREMGVEIISCTVDRDTCVCGCKKQYRHWSENLFQCFNCSCLNGTVHLSQCE 120  
DB 61 SCSSKREMGVEIISCTVDRDTCVCGCKKQYRHWSENLFQCFNCSCLNGTVHLSQCE 120  
QY 121 KONTVCTCHAGFFLENECVSCNCKRKSLECTCTLCPOIEN 161  
DB 121 KONTVCTCHAGFFLENECVSCNCKRKSLECTCTLCPOIEN 161  
RESULT 3  
US-09-792-356-4  
Sequence 4, Application US/09792356  
Patent No. US20020183485A1  
GENERAL INFORMATION:  
APPLICANT: Hauptmann, Rudolph  
APPLICANT: Hummeler, Adolph  
APPLICANT: Maurer-Fogy, Ingrid  
APPLICANT: Stratowa, Christian  
TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for  
FILE REFERENCE: 98,385-G  
CURRENT APPLICATION NUMBER: US/09/792,356  
CURRENT FILING DATE: 2001-08-17  
PRIOR APPLICATION NUMBER: 08/477,639

QY 121 KONTVCTCHAGFFLENECVSCNCKRKSLECTCTLCPOIEN 161  
DB 61 SCSSKREMGVEIISCTVDRDTCVCGCKKQYRHWSENLFQCFNCSCLNGTVHLSQCE 120  
QY 61 SCSSKREMGVEIISCTVDRDTCVCGCKKQYRHWSENLFQCFNCSCLNGTVHLSQCE 120  
DB 61 SCSSKREMGVEIISCTVDRDTCVCGCKKQYRHWSENLFQCFNCSCLNGTVHLSQCE 120  
QY 121 KONTVCTCHAGFFLENECVSCNCKRKSLECTCTLCPOIEN 161  
DB 121 KONTVCTCHAGFFLENECVSCNCKRKSLECTCTLCPOIEN 161  
RESULT 4  
US-09-899-422-4  
Sequence 4, Application US/09899422  
Patent No. US20020090676A1  
GENERAL INFORMATION:  
APPLICANT: Hauptmann, Rudolph  
APPLICANT: Hummeler, Adolph  
APPLICANT: Maurer-Fogy, Ingrid  
APPLICANT: Stratowa, Christian  
TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for  
FILE REFERENCE: 98,385-H  
CURRENT APPLICATION NUMBER: US/09/899,422  
CURRENT FILING DATE: 2001-08-21  
PRIOR APPLICATION NUMBER: 09/525,998  
PRIOR FILING DATE: 2000-03-15  
PRIOR APPLICATION NUMBER: 08/383,676  
PRIOR FILING DATE: 1995-02-01  
PRIOR APPLICATION NUMBER: 08/153,287  
PRIOR FILING DATE: 1993-11-17  
PRIOR APPLICATION NUMBER: 07/821,750  
PRIOR FILING DATE: 1992-01-02  
PRIOR APPLICATION NUMBER: 07/511,430  
PRIOR FILING DATE: 1990-04-20  
NUMBER OF SEQ ID NOS: 87  
SOFTWARE: Patent In Ver. 2.0  
SEQ ID NO 4  
LENGTH: 161  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-899-422-4  
Query Match 100.0%; Score 941; DB 10; Length 161;  
Best Local Similarity 100.0%; Pred. No. 2.8e-61;  
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 121 KONTVCTCHAGFFLENECVSCNCKRKSLECTCTLCPOIEN 161  
DB 61 SCSSKREMGVEIISCTVDRDTCVCGCKKQYRHWSENLFQCFNCSCLNGTVHLSQCE 120  
QY 61 SCSSKREMGVEIISCTVDRDTCVCGCKKQYRHWSENLFQCFNCSCLNGTVHLSQCE 120  
DB 61 SCSSKREMGVEIISCTVDRDTCVCGCKKQYRHWSENLFQCFNCSCLNGTVHLSQCE 120  
QY 121 KONTVCTCHAGFFLENECVSCNCKRKSLECTCTLCPOIEN 161  
DB 121 KONTVCTCHAGFFLENECVSCNCKRKSLECTCTLCPOIEN 161  
RESULT 5  
US-09-792-356-4  
Sequence 4, Application US/09792356  
Patent No. US20020183485A1  
GENERAL INFORMATION:  
APPLICANT: Hauptmann, Rudolph  
APPLICANT: Hummeler, Adolph  
APPLICANT: Maurer-Fogy, Ingrid  
APPLICANT: Stratowa, Christian  
TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for  
FILE REFERENCE: 98,385-G  
CURRENT APPLICATION NUMBER: US/09/792,356  
CURRENT FILING DATE: 2001-08-17  
PRIOR APPLICATION NUMBER: 08/477,639



QY 61 SCSEKPEKMGQVEISSCTVDRPTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 120  
Db 61 SCSEKPEKMGQVEISSCTVDRPTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 120  
QY 121 KQNTVCTCHAGFFLPENECVSCSNCKYSLECTKLCLOPIEN 161  
Db 121 KQNTVCTCHAGFFLPENECVSCSNCKYSLECTKLCLOPIEN 161

RESULT 5  
US-09 907-263-2  
Sequence 2, Application US/0907263  
Patent No. US20020119924A1  
GENERAL INFORMATION:  
APPLICANT: Bendelle, Alison M.  
Sennello, Regina M.  
Edwards, Carl K.

TITLE OF INVENTION: COMBINATION THERAPY USING A TNF BINDING  
PROTEIN FOR TREATING TNF-MEDIATED DISEASES  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Amgen Inc.  
STREET: 1840 DeHavilland Drive  
CITY: Thousand Oaks  
STATE: CA  
COUNTRY: US  
ZIP: 91320-1789

COMPUTER PFADABLE FORM.  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/907,263  
FILING DATE: 17-Jul-2001  
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 09/326,394  
FILING DATE: 1999-06-04  
APPLICATION NUMBER: US 60/036,355  
FILING DATE: 23-JAN-1997  
APPLICATION NUMBER: US 60/039,315  
FILING DATE: 07-FEB-1997  
APPLICATION NUMBER: US 60/052,023  
FILING DATE: 09-JUL-1997

ATTORNEY/AGENT INFORMATION:  
NAME: Zindrick, Thomas K.  
REGISTRATION NUMBER: 32,185  
REFERENCE/DOCKET NUMBER: A-430D  
INFORMATION FOR SEQ ID NO: 2  
SEQUENCE CHARACTERISTICS:  
LENGTH: 161 amino acids  
TYPE: amino acid  
TOPOLOGY: linear

MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
US 09 907 263-2

Query Match 100.0%; Score 941; DB 10; Length 161;  
Best Local Similarity 100.0%; Pred. No. 2.8e-61;  
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSVCPQGGKYIHPQNNISCTCTKCHKFTYLYNDCPGSDTDCPECSGFTASENHLRHCL 60  
Db 1 DSVCPQGGKYIHPQNNISCTCTKCHKFTYLYNDCPGSDTDCPECSGFTASENHLRHCL 60  
QY 61 SCSEKPEKMGQVEISSCTVDRPTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 120  
Db 61 SCSEKPEKMGQVEISSCTVDRPTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 120

QY 121 KQNTVCTCHAGFFLPENECVSCSNCKYSLECTKLCLOPIEN 161  
Db 121 KQNTVCTCHAGFFLPENECVSCSNCKYSLECTKLCLOPIEN 161

Db 121 KQNTVCTCHAGFFLPENECVSCSNCKYSLECTKLCLOPIEN 161

RESULT 6  
US-09-899-429A-6  
Sequence 6, Application US/0909429A  
Patent No. US20020169118A1  
GENERAL INFORMATION:  
APPLICANT: Hauptmann, Rudolph  
Himmeler, Adolph  
Maurer-Foggy, Ingrid  
Stratowa, Christian

TITLE OF INVENTION: TNF Receptors, The Binding Proteins and Pore Binding for  
TITLE OF INVENTION: TNF Receptors, The Binding Proteins and Pore Binding for  
FILE REFERENCE: 98-385-J  
CURRENT APPLICATION NUMBER: US/09/899,429A  
CURRENT FILING DATE: 2001-07-03  
PRIOR APPLICATION NUMBER: 09/792,356  
PRIOR FILING DATE: 2000-02-23  
PRIOR APPLICATION NUMBER: 08/477,639  
PRIOR FILING DATE: 1995-06-07  
PRIOR APPLICATION NUMBER: 08/383,676  
PRIOR FILING DATE: 1995-02-01  
PRIOR APPLICATION NUMBER: 08/153,287  
PRIOR FILING DATE: 1993-11-17  
PRIOR APPLICATION NUMBER: 07/821,750  
PRIOR FILING DATE: 1992-01-02  
PRIOR APPLICATION NUMBER: 07/511,430  
PRIOR FILING DATE: 1990-04-20  
NUMBER OF SEQ ID NOS: 97  
SOFTWARE: Patent In Ver. 2.0  
SEQ ID NO 6

LENGTH: 162  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: recombinant  
OTHER INFORMATION: TNF-PP sequence  
US-09-899-429A-6

Query Match 100.0%; Score 941; DB 9; Length 162;  
Best Local Similarity 100.0%; Pred. No. 2.8e-61;  
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSVCPQGGKYIHPQNNISCTCTKCHKFTYLYNDCPGSDTDCPECSGFTASENHLRHCL 60  
Db 2 DSVCPQGGKYIHPQNNISCTCTKCHKFTYLYNDCPGSDTDCPECSGFTASENHLRHCL 61  
QY 61 SCSEKPEKMGQVEISSCTVDRPTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 120  
Db 62 SCSEKPEKMGQVEISSCTVDRPTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQE 121

QY 121 KQNTVCTCHAGFFLPENECVSCSNCKYSLECTKLCLOPIEN 161  
Db 122 KQNTVCTCHAGFFLPENECVSCSNCKYSLECTKLCLOPIEN 162

RESULT 7  
US-09-798-789-9  
Sequence 9, Application US/09798789  
Patent No. US20020009780A1  
GENERAL INFORMATION:  
APPLICANT: Dahiyat, Bassil  
Filikov, Anton  
TITLE OF INVENTION: DESIGN AND DISCOVERY OF PROTEIN BASED TNF ALPHA  
TITLE OF INVENTION: VARIANTS FOR THE TREATMENT OF TNF-ALPHA RELATED  
FILE REFERENCE: A-68990-1/RFT/RMS/BMK  
CURRENT APPLICATION NUMBER: US/09/798,789  
CURRENT FILING DATE: 2001-03-02  
PRIOR APPLICATION NUMBER: US 60/186,427  
PRIOR FILING DATE: 2000-03-02  
NUMBER OF SEQ ID NOS: 22

SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 9  
LENGTH: 162  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-798-789-9

Query Match 100.0%; Score 941; DB 10; Length 162;  
Best Local Similarity 100.0%; Pred. No. 2, Re-61;  
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LSVCEGQGYIHPQNNISICTCKHKGTYLYNDGPGQDTCRECGSGFTASENHLRHCL 60  
DB 2 LSVCEGQGYIHPQNNISICTCKHKGTYLYNDGPGQDTCRECGSGFTASENHLRHCL 61  
QY 61 SCSKREMGQVEISSCTVDRDTCVCGCRKQYRHYWSENLFQCFNCSLCLNGTVHLSQCE 120  
DB 62 SCSKREMGQVEISSCTVDRDTCVCGCRKQYRHYWSENLFQCFNCSLCLNGTVHLSQCE 121  
QY 121 KQNTVCTCHAGFLPENEVCVCSNCKSKLECTKLCPLQIEN 161  
DB 122 KQNTVCTCHAGFLPENEVCVCSNCKSKLECTKLCPLQIEN 162

RESULT 8  
US-09-798-789-22  
Sequence 22, Application US/09798789  
Patent No. US2002009780A1  
GENERAL INFORMATION:  
APPLICANT: Dahiya, Basill  
APPLICANT: Filikov, Anton  
TITLE OF INVENTION: DESIGN AND DISCOVERY OF PROTEIN BASED TNF-ALPHA  
TITLE OF INVENTION: VARIANTS FOR THE TREATMENT OF TNF-ALPHA RELATED  
TITLE OF INVENTION: DISORDERS  
FILE REFERENCE: A-68990-1/RT/RMS/RMK  
CURRENT APPLICATION NUMBER: US/09/798, 789  
CURRENT FILING DATE: 2001-03-02  
PRIORITY FILING DATE: 2000-03-02  
PRIORITY FILING DATE: 2000-03-02  
NUMBER OF SEQ ID NOS: 22  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 22  
LENGTH: 162  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE: Artificial Sequence  
OTHER INFORMATION: Description of Artificial Sequence: synthetic  
US-09-798-789-22

Query Match 100.0%; Score 941; DB 10; Length 162;  
Best Local Similarity 100.0%; Pred. No. 2, Re-61;  
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LSVCEGQGYIHPQNNISICTCKHKGTYLYNDGPGQDTCRECGSGFTASENHLRHCL 60  
DB 2 LSVCEGQGYIHPQNNISICTCKHKGTYLYNDGPGQDTCRECGSGFTASENHLRHCL 61  
QY 61 SCSKREMGQVEISSCTVDRDTCVCGCRKQYRHYWSENLFQCFNCSLCLNGTVHLSQCE 120  
DB 62 SCSKREMGQVEISSCTVDRDTCVCGCRKQYRHYWSENLFQCFNCSLCLNGTVHLSQCE 121  
QY 121 KQNTVCTCHAGFLPENEVCVCSNCKSKLECTKLCPLQIEN 161  
DB 122 KQNTVCTCHAGFLPENEVCVCSNCKSKLECTKLCPLQIEN 162

RESULT 9  
US-09-899-429A-20  
Sequence 20, Application US/09899429A  
Patent No. US20020169118A1  
GENERAL INFORMATION:  
APPLICANT: Hauptmann, Rudolph  
APPLICANT: Himmeler, Adolph  
US-09-899-429A-20

APPLICANT: Maurer-Fogy, Ingrid  
APPLICANT: Stratowa, Christian  
TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for  
TITLE OF INVENTION: Them  
FILE REFERENCE: 98-385-J  
CURRENT APPLICATION NUMBER: US/09/899,429A  
CURRENT FILING DATE: 2001-07-03  
PRIOR APPLICATION NUMBER: 09/732,356  
PRIOR FILING DATE: 2000-02-23  
PRIOR APPLICATION NUMBER: 08/477,639  
PRIOR FILING DATE: 1995-06-07  
PRIOR APPLICATION NUMBER: 08/383,676  
PRIOR FILING DATE: 1995-02-01  
PRIOR APPLICATION NUMBER: 08/153,287  
PRIOR FILING DATE: 1993-11-17  
PRIOR APPLICATION NUMBER: 07/821,750  
PRIOR FILING DATE: 1992-01-02  
PRIOR APPLICATION NUMBER: 07/511,430  
PRIOR FILING DATE: 1990-04-20  
NUMBER OF SEQ ID NOS: 97  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 20  
LENGTH: 172  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE: Artificial Sequence  
OTHER INFORMATION: Description of Artificial Sequence: recombinant  
OTHER INFORMATION: TNF-BP sequence  
US-09-899-429A-20

Query Match 100.0%; Score 941; DB 9; Length 172;  
Best Local Similarity 100.0%; Pred. No. 3e-61;  
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSVCEGQGYIHPQNNISICTCKHKGTYLYNDGPGQDTCRECGSGFTASENHLRHCL 60  
DB 2 LSVCEGQGYIHPQNNISICTCKHKGTYLYNDGPGQDTCRECGSGFTASENHLRHCL 61  
QY 61 SCSKREMGQVEISSCTVDRDTCVCGCRKQYRHYWSENLFQCFNCSLCLNGTVHLSQCE 120  
DB 62 SCSKREMGQVEISSCTVDRDTCVCGCRKQYRHYWSENLFQCFNCSLCLNGTVHLSQCE 121  
QY 121 KQNTVCTCHAGFLPENEVCVCSNCKSKLECTKLCPLQIEN 161  
DB 122 KQNTVCTCHAGFLPENEVCVCSNCKSKLECTKLCPLQIEN 162

RESULT 10  
US-09-899-429A-16  
Sequence 16, Application US/09899429A  
Patent No. US20020169118A1  
GENERAL INFORMATION:  
APPLICANT: Hauptmann, Rudolph  
APPLICANT: Himmeler, Adolph  
APPLICANT: Maurer-Fogy, Ingrid  
APPLICANT: Stratowa, Christian  
TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for  
TITLE OF INVENTION: Them  
FILE REFERENCE: 98-385-J  
CURRENT APPLICATION NUMBER: US/09/899,429A  
CURRENT FILING DATE: 2001-07-03  
PRIOR APPLICATION NUMBER: 09/732,356  
PRIOR FILING DATE: 2000-02-23  
PRIOR APPLICATION NUMBER: 08/477,639  
PRIOR FILING DATE: 1995-06-07  
PRIOR APPLICATION NUMBER: 08/383,676  
PRIOR FILING DATE: 1995-02-01  
PRIOR APPLICATION NUMBER: 08/153,287  
PRIOR FILING DATE: 1993-11-17  
PRIOR APPLICATION NUMBER: 07/821,750  
PRIOR FILING DATE: 1992-01-02  
PRIOR APPLICATION NUMBER: 07/511,430  
PRIOR FILING DATE: 1990-04-20

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; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 16
; LENGTH: 173
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: recombinant
; OTHER INFORMATION: TNF-BP sequence
US 09 899 429A 16

Query Match 100.0%; Score 941; DB 9; Length 173;
Best Local Similarity 100.0%; Pred. No. 3e-61;
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSVCPQGVYHPQNNISCTTKHKTYLYNDGPGQDTDCPEESGFTASENHLPHCL 60
DB 13 DSVCPQGVYHPQNNISCTTKHKTYLYNDGPGQDTDCPEESGFTASENHLPHCL 72

QY 61 SCSKCPKEMGQVEISSCTVDPTVCGPKNQYRHYWSENLPQCFCNCSLCLNGTIVHLSQCF 120
DB 73 SCSKCPKEMGQVEISSCTVDPTVCGPKNQYRHYWSENLPQCFCNCSLCLNGTIVHLSQCF 132

QY 121 KQNTVCTCHAGFFLPENECVSCNCKKYSLECTKLCLOPIEN 161
DB 133 KQNTVCTCHAGFFLPENECVSCNCKKYSLECTKLCLOPIEN 173

RESULT 11
US-09-899-429A-10
; Sequence 10, Application US/09899429A
; Patent No. US20020169118A1
; GENERAL INFORMATION:
; APPLICANT: Hauptmann, Rudolph
; APPLICANT: Himmler, Adolph
; APPLICANT: Maurer-Fogy, Ingrid
; APPLICANT: Stratowa, Christian
; TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for
; FILE REFERENCE: 98-385-J
; CURRENT APPLICATION NUMBER: US/09/899,429A
; PRIOR FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: 09/792,356
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 08/477,639
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 08/383,676
; PRIOR FILING DATE: 1995-02-01
; PRIOR APPLICATION NUMBER: 08/153,287
; PRIOR FILING DATE: 1993-11-17
; PRIOR APPLICATION NUMBER: 07/821,750
; PRIOR FILING DATE: 1992-01-02
; PRIOR APPLICATION NUMBER: 07/511,430
; PRIOR FILING DATE: 1990-04-20
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 18
; LENGTH: 190
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: recombinant
; OTHER INFORMATION: TNF-BP sequence
US-09-899-429A-10

Query Match 100.0%; Score 941; DB 9; Length 183;
Best Local Similarity 100.0%; Pred. No. 3.1e-61;
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSVCPQGVYHPQNNISCTTKHKTYLYNDGPGQDTDCPEESGFTASENHLPHCL 60
DB 13 DSVCPQGVYHPQNNISCTTKHKTYLYNDGPGQDTDCPEESGFTASENHLPHCL 72

QY 61 SCSKCPKEMGQVEISSCTVDPTVCGPKNQYRHYWSENLPQCFCNCSLCLNGTIVHLSQCF 120
DB 73 SCSKCPKEMGQVEISSCTVDPTVCGPKNQYRHYWSENLPQCFCNCSLCLNGTIVHLSQCF 132

QY 121 KQNTVCTCHAGFFLPENECVSCNCKKYSLECTKLCLOPIEN 161
DB 133 KQNTVCTCHAGFFLPENECVSCNCKKYSLECTKLCLOPIEN 173

RESULT 12
US-09-899-429A-18
; Sequence 18, Application US/09899429A
; Patent No. US20020169118A1
; GENERAL INFORMATION:
; APPLICANT: Hauptmann, Rudolph
; APPLICANT: Himmler, Adolph
; APPLICANT: Maurer-Fogy, Ingrid
; APPLICANT: Stratowa, Christian
; TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for
; FILE REFERENCE: 98-385-J
; CURRENT APPLICATION NUMBER: US/09/899,429A
; PRIOR FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: 09/792,356
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 08/477,639
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 08/383,676
; PRIOR FILING DATE: 1995-02-01
; PRIOR APPLICATION NUMBER: 08/153,287
; PRIOR FILING DATE: 1993-11-17
; PRIOR APPLICATION NUMBER: 07/821,750
; PRIOR FILING DATE: 1992-01-02
; PRIOR APPLICATION NUMBER: 07/511,430
; PRIOR FILING DATE: 1990-04-20
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 18
; LENGTH: 190
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: recombinant
; OTHER INFORMATION: TNF-BP sequence
US-09-899-429A-18

Query Match 100.0%; Score 941; DB 9; Length 190;
Best Local Similarity 100.0%; Pred. No. 3.2e-61;
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSVCPQGVYHPQNNISCTTKHKTYLYNDGPGQDTDCPEESGFTASENHLPHCL 60
DB 30 DSVCPQGVYHPQNNISCTTKHKTYLYNDGPGQDTDCPEESGFTASENHLPHCL 89

QY 61 SCSKCPKEMGQVEISSCTVDPTVCGPKNQYRHYWSENLPQCFCNCSLCLNGTIVHLSQCF 120
DB 90 SCSKCPKEMGQVEISSCTVDPTVCGPKNQYRHYWSENLPQCFCNCSLCLNGTIVHLSQCF 149

QY 121 KQNTVCTCHAGFFLPENECVSCNCKKYSLECTKLCLOPIEN 161
DB 150 KQNTVCTCHAGFFLPENECVSCNCKKYSLECTKLCLOPIEN 190

RESULT 13
US-09-899-429A-12
; Sequence 12, Application US/09899429A
; Patent No. US20020169118A1
; GENERAL INFORMATION:
; APPLICANT: Hauptmann, Rudolph
; APPLICANT: Himmler, Adolph
; APPLICANT: Maurer-Fogy, Ingrid
; APPLICANT: Stratowa, Christian
; TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for
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Search completed: January 6, 2003, 04:00:32  
Job time : 15 secs

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A:Residues: 1-455 <GRA>  
 A:Cross-references: GB:M37764  
 A:Note: the authors translated the codon TGG for residue 371 as Thr, AAG for residue 372 as Arg, and the authors translated the codon TGG for residue 371 as Thr, AAG for residue 372 as Arg, and the authors translated the codon TGG for residue 371 as Thr, AAG for residue 372 as Arg.  
 A:Title: Soluble forms of tumor necrosis factor receptors (TNF-Rs). The cDNA for the type I form of the receptor.  
 A:Reference number: S12057; MUID:91006021; PMID:1698610  
 A:Accession: S12057  
 A:Molecule type: mRNA  
 A:Residues: 1-455 <NRN>  
 A:Cross-references: EMBL:X55313; NID:937223; PIDD:CA19021.1; PIDD:937224  
 A:Note: parts of soluble TNF binding protein 1, including its amino and carboxyl ends, were cloned from a cDNA library.  
 A:Title: Cloning and partial characterization of the promoter for the human p55 tumor necrosis factor receptor.  
 A:Reference number: J0758; MUID:94055779; PMID:8262379  
 A:Accession: J0758  
 A:Molecule type: DNA  
 A:Residues: 1-13 <KEM>  
 A:Sequence: P. Vey, E. Turcatti, G. Wingfield, P. Dayer, J.M.  
 Eur. J. Immunol. 20, 1167-1174, 1990  
 A:Title: Tumor necrosis factor inhibitor: purification, NH-2-terminal amino acid sequence, and characterization of an inhibitor (soluble tumor necrosis factor inhibitor).  
 A:Reference number: A60331; MUID:90292116; PMID:2113477  
 A:Accession: A60331  
 A:Molecule type: protein  
 A:Residues: 41-43, 'X', 45-53, 'X', 55-57, 'XK', 60 <OLS>  
 A:Cross-references: T. Hwang, C. Koh, W. Cappuccini, F. Lucii III, J.A. Jeffes, E.W.B. De  
 Proc. Natl. Acad. Sci. U.S.A. 87, 8781-8784, 1990  
 A:Title: Purification and characterization of an inhibitor (soluble tumor necrosis factor inhibitor).  
 A:Reference number: A39258; MUID:9106364; PMID:2174164  
 A:Accession: A39258  
 A:Molecule type: protein  
 A:Residues: 41-60 <GAT>  
 A:Experimental source: cancer patient serum  
 A:Reference number: A15010; MUID:90112315; PMID:2153136  
 A:Title: Two tumor necrosis factor-binding proteins purified from human urine. Evidence for a common binding site.  
 A:Reference number: J02404; MUID:95128033; PMID:7765720  
 A:Accession: J02404  
 A:Molecule type: protein  
 A:Residues: 41-45 <ENG>  
 A:Experimental source: normal urine  
 A:Reference number: J02404; MUID:95128033; PMID:7765720  
 A:Title: Amino acid sequence of natural tumor necrosis factor alpha inhibitor purified from human urine.  
 A:Reference number: J02404; MUID:95128033; PMID:7765720  
 A:Accession: J02404  
 A:Molecule type: protein  
 A:Residues: 41-53, 'X', 55-144, 'X', 146-150, 'X', 152-186, 'X', 188-201 <KAL>  
 A:Experimental source: urine  
 A:Note: This protein is one of two known receptors for both TNF-alpha (cachectin) and TNF-beta (lymphotoxin).  
 A:Gene: GDB:TNFR1  
 A:Cross-references: CDB:125313; OMIM:191190  
 A:Map position: 12p13.2-12p13.3  
 A:Introns: 13/5, 65/1, 108/1, 158/1, 184/2, 209/1, 247/1, 256/3, 353/1  
 A:Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology  
 A:Keywords: duplication, glycoprotein, receptor, transmembrane protein  
 F:1-21/Domain: signal sequence #status predicted <SIG>  
 F:22-455/Product: tumor necrosis factor receptor 1 #status predicted <EXT>  
 F:30-211/Domain: extracellular #status predicted <EXT>  
 F:41-201/Product: TNF binding protein 1 (tumor necrosis factor alpha inhibitor) #status predicted <EXT>  
 F:44-82/Domain: NGF receptor repeat homology <NGI>

F:84-126/Domain: NGF receptor repeat homology <NG2>  
 F:127-167/Domain: NGF receptor repeat homology <NG3>  
 F:168-196/Domain: NGF receptor repeat homology <NG4>  
 F:216-234/Domain: transmembrane #status predicted <MEM>  
 F:235-455/Domain: intracellular #status predicted <INT>  
 F:54-145,151/binding site: carbohydrate (Asn) (covalent) #status predicted  
 Query Match 100.0%; Score 941; DB 1; Length 455;  
 Best Local Similarity 77.4%; Pred. No. 8,3e-62;  
 Matches 161, Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Query 1 DSVCPGKXYTHPNNNSICTCKHKGTYLYNDGPGQDDTDCBESGSGFTASENHLRCL 60  
 Db 41 DSVCPGKXYTHPNNNSICTCKHKGTYLYNDGPGQDDTDCBESGSGFTASENHLRCL 100  
 Query 61 SCSKCRKEMGVEISSCTVDRTVCGCRKQYRHWSENLFCFNCISLNTVHLSQCE 120  
 Db 101 SCSKCRKEMGVEISSCTVDRTVCGCRKQYRHWSENLFCFNCISLNTVHLSQCE 160  
 Query 121 KQNTVCTCHAGFFLRNECVSCNCKKSLECTKCLPDIEN 161  
 Db 161 KQNTVCTCHAGFFLRNECVSCNCKKSLECTKCLPDIEN 201  
 RESULT 2  
 JC4302  
 Tumor necrosis factor receptor p55 precursor - pig  
 C:Species: Sus scrofa domestica (domestic pig)  
 C>Date: 29-Nov-1995 #sequence\_revision 08-Feb-1996 #text\_change 23-Jul-1999  
 A:Accession: JC4302; MUID:9601645; PMID:7530278  
 A:Residues: 1-461 <SUT>  
 A:Molecule type: mRNA  
 A:Cross-references: GB:U19994; NID:3141752; PIDD:AA048499.1; FID:3141753  
 A:Accession: PC4093  
 A:Molecule type: protein  
 A:Residues: 1-7 <SUT>  
 A:Experimental source: kidney cell line 15  
 A:Gene: tnfr  
 C:Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology  
 C:Keywords: glycoprotein, kidney, receptor, transmembrane protein, tumor  
 F:1-29/Domain: signal sequence #status predicted <SIG>  
 F:30-461/Product: tumor necrosis factor receptor p55 #status predicted <MAT>  
 F:44-194/Domain: extracellular cysteine rich #status predicted <EXT>  
 F:44-126/Domain: NGF receptor repeat homology <NGF>  
 F:211-231/Domain: transmembrane #status predicted <MEM>  
 F:361-447/Domain: signal transduction #status predicted <SIT>  
 F:54-145,151/binding site: carbohydrate (Asn) (covalent) #status predicted  
 Query Match 76.1%; Score 716.5; DB 2; Length 461;  
 Best Local Similarity 77.4%; Pred. No. 3e-45;  
 Matches 120, Conservative 12, Mismatches 23, Indels 1; Gaps 1;  
 Query 1 DSVCPGKXYTHPNNNSICTCKHKGTYLYNDGPGQDDTDCBESGSGFTASENHLRCL 60  
 Db 41 DSVCPGKXYTHPNNNSICTCKHKGTYLYNDGPGQDDTDCBESGSGFTASENHLRCL 100  
 Query 61 SCSKCRKEMGVEISSCTVDRTVCGCRKQYRHWSENLFCFNCISLNTVHLSQCE 120  
 Db 101 SCSKCRKEMGVEISSCTVDRTVCGCRKQYRHWSENLFCFNCISLNTVHLSQCE 160  
 Query 121 KQNTVCTCHAGFFLRNECVSCNCKKSLECTKCLPDIEN 155  
 Db 161 KQNTVCTCHAGFFLRNECVSCNCKKSLECTKCLPDIEN 194  
 RESULT 3





A:Reference number: 154182; MUID:93252381; PMID:8486360  
 A:Accession: 154182  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-435 <RES>  
 A:Cross-references: GB:L04270; NID:g339761; PIR:AAA36757.1; PIR:g339762  
 C:Genetics:  
 A:Gene: GDB:LTBR  
 A:Cross-references: GDB:1230195; OMIM:600979  
 A:Map position: 17q21.31-32  
 A:Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology

Query Match 19.9%; Score 187.5; DB 2; Length 435;  
 Best Local Similarity 32.7%; Pred. No. 7.4e-07;  
 Matches 49; Conservative 17; Mismatches 71; Indels 13; Gaps 7;

QY 8 FYHFNANSICCTKCKGTYLYNDGPGQDDTDCREC-ESGSFTASENHLRLCLSC 67  
 DB 49 EYEPQHR-IGCSRCPEPTYSAK-SPIPTVCATCATKSNYNHMYLTICQLCRCPD 106  
 C: 68 EWGVETSSCTVLPRTVQCPENYEHWSNLPQCNCS-CLNGVHLSCQE-KQ 122  
 DB 107 VMLEELIACVTSKKTQCPQPMFCMAWA--LECHCELLSDCPQTEALKDEVGKG 163  
 QY 23 NTWC-CHAGFPLERECEVGCNSCKSLFC 151  
 DB 164 NMHCVPYAGHP--QNTSSPSARCPHTRC 191

RESULT 6  
 COHUN  
 nerve growth factor receptor precursor, low affinity [validated] - human  
 N:Alternate names: NGF receptor  
 C:Species: Homo sapiens (man)  
 C:Date: 31-Mar-1988 #sequence, revision 31-Mar-1988 #text\_change 08-Dec-2000  
 C:Accession: A05228, A60204, S21683, S216838  
 P:Johnson, D.; Latham, A.; Ruck, C.P.; Sehgal, A.; Morgan, C.; Mercer, E.; Bothwell, M.  
 Cell 47, 545-554, 1986  
 A:Title: Expression and structure of the human NGF receptor.  
 A:Reference number: A05228; MUID:8705725; PMID:3022937  
 A:Accession: A05228  
 A:Molecule type: mRNA  
 A:Residues: 1-427 <JOB>  
 A:Cross-references: GB:M4764; NID:g189204; PIR:AA59544.1; PIR:g189205  
 P:Marano, N.; Dierschold, B.; Earley Jr., J.J.; Schaltenman, G.; Thompson, S.; Grob, P.;  
 J. Neurosci. 48, 225-233, 1987  
 A:Title: Purification and amino terminal sequencing of human melanoma nerve growth facto  
 A:Reference number: A60204; MUID:8708574; PMID:3025363  
 A:Accession: A60204  
 A:Molecule type: Protein  
 A:Residues: 29, 31, 33, 42, 44, 45, 46, 47, 50-51, 54-56 <MAR>  
 A:Experimental source: melanoma cell line A875  
 A:Note: this sequence has been corrected by a note added in proof to follow the nucleoti  
 R:Visvader, J., P.; Leszyk, J.D.; Lin-Goerke, J.; Ross, A.H.  
 Arch. Biochem. Biophys. 234, 244-252, 1992  
 A:Title: Structural domains of the extracellular domain of human nerve growth factor rec  
 A:Reference number: S21689; MUID:92198017; PMID:1372492  
 A:Accession: S21689  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 183-208 <VIS>  
 R:Sehgal, A.; Patil, N.; Chao, M.  
 Mol. Cell. Biol. 8, 3160-3167, 1988  
 A:Title: A constitutive promoter directs expression of the nerve growth factor receptor  
 A:Reference number: 157638; MUID:89096903; PMID:2650481  
 A:Accession: 157638  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-22 <RES>  
 A:Cross-references: GB:M1621; NID:g189206; PIR:AA36363.1; PIR:g189207  
 C:Comment: This receptor is found on sensory and sympathetic neurons, on neuroblastoma c  
 C:Comment: The cysteine-rich region of the extracellular domain may form part or all of  
 C:Comment: This protein is thought to form a high-affinity receptor when it associates w

C:Comment: This receptor undergoes both N- and O-linked glycosylation.  
 C:Genetics:  
 A:Gene: GDB:NGFR  
 A:Cross-references: GDB:120234; OMIM:162010  
 A:Map position: 17q21.31-32  
 C:Superfamily: nerve growth factor receptor; NGF receptor repeat homology  
 C:Keywords: duplication; glycoprotein; heterodimer; monomer; phosphoprotein; receptor;  
 F:1-28/Domain: signal sequence #status predicted <SIG>  
 F:29-427/Product: nerve growth factor receptor #status experimental <MAT>  
 F:29-250/Domain: extracellular #status predicted <EXT>  
 F:32-65/Domain: NGF receptor repeat homology <NG1>  
 F:67-108/Domain: NGF receptor repeat homology <NG2>  
 F:103-147/Domain: NGF receptor repeat homology <NG3>  
 F:143-189/Domain: NGF receptor repeat homology <NG4>  
 F:197-248/Region: serine/threonine-rich  
 F:251-272/Domain: transmembrane #status predicted <TRM>  
 F:273-447/Domain: intracellular #status predicted <INT>  
 F:60/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 19.4%; Score 182.5; DB 1; Length 427;  
 Best Local Similarity 32.1%; Pred. No. 1.7e-06;  
 Matches 52; Conservative 25; Mismatches 62; Indels 23; Gaps 11;

QY 4 CPOGVIHPONNSICCTKCKGTYLYNDGPGQDDTDCREC-ESGSFTASENHLRLCLSC 62  
 DB 32 CPTGLYTH--SGSCCAKALGEGVAQC-GANQ-TVCEPCLDSTVSVAATEPCPC 86  
 QY 63 SKCRKMGQVEISS-CTVDRDTVCGCRKNQRYHWSNLPQCNCSCLNGT-VHLSCQE 120  
 DB 87 TEC--VQLGMSAPCVEADDAVCRG--AYGYQDETTRGCRACVCEAGSLVFSSCD 140  
 QY 121 KONTVC-TCHAGFPLER---NECVGSNC---KSLCCTK 153  
 DB 141 KONTVCBCPDGYTSDANHVDPCLPTVCEDETRQLRECTR 182

RESULT 7  
 B38634  
 tumor necrosis factor receptor type 2 precursor - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 30-Jun-1992 #sequence, revision 30 Jun-1992 #text\_change 23-Jul-1999  
 C:Accession: B38634; A40254; S54816  
 R:Leewis, M.; Tartaglia, L.A.; Lee, A.; Bennett, G.L.; Rice, G.C.; Wong, G.H.W.; Chen, E  
 Proc. Natl. Acad. Sci. U.S.A. 88, 2830-2834, 1991  
 A:Title: Cloning and expression of cDNAs for two distinct murine tumor necrosis factor r  
 A:Reference number: A38634; MUID:91187885; PMID:1843278  
 A:Accession: B38634  
 A:Molecule type: mRNA  
 A:Residues: 1-474 <LEW>  
 A:Cross-references: GB:M60469; NID:g199827; PIR:AAA39752.1; PIR:g199828  
 R:Goodwin, R.G.; Anderson, D.; Jerzy, R.; Davis, T.; Bradman, C.T.; Copeland, N.G.; Jenk  
 Mol. Cell. Biol. 11, 3020-3026, 1991  
 A:Title: Molecular cloning and expression of the type 1 and type 2 murine receptors for  
 A:Reference number: A40254; MUID:91246168; PMID:1645445  
 A:Accession: A40254  
 A:Molecule type: mRNA  
 A:Residues: 1-474 <GOO>  
 A:Cross-references: GB:M60469; NID:g199827; PIR:AAA39752.1; PIR:g199828  
 R:Kisssnerghis, M.; Felloes, R.; Feldmann, M.; Chetnaovsky, Y.  
 submitted to the EMBL Data Library, May 1995  
 A:Description: Characterization of the promoter region of the murine p75-TNF receptor.  
 A:Reference number: S54816  
 A:Accession: S54816  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-22 <KIS>  
 A:Cross-references: EMBL:X87128; NID:g809043; PIR:CAA60618.1; PIR:g809044  
 C:Superfamily: tumor necrosis factor receptor type 2; NGF receptor repeat homology  
 C:Keywords: cytokine receptor; transmembrane protein  
 F:1-22/Domain: signal sequence #status predicted <SIG>  
 F:23-474/Product: tumor necrosis factor receptor type 2 #status predicted <MAT>  
 F:40-77/Domain: NGF receptor repeat homology <NG1>  
 F:79-120/Domain: NGF receptor repeat homology <NG2>

F:166 201/Domain: NGF receptor repeat homology <NG4>

Query Match 19.2% Score 181; DB 2; Length 474;  
Best Local Similarity 31.7% Pred. No. 2 3e-06;  
Matches 51; Conservative 20; Mismatches 76; Indels 14; Gaps 8;

QY 4 QPGQYVHPPNNISICTYCHKGTLYNDGPGQDTPCEGSGFTASENHLPCHLSC 62  
DB 40 COISQRYVDRKACMCAPPPQYVYKHC-NKTSDTVCADCEASMYTCVMNPPTCLSCS 98  
QY 63 SKCPKEMQVEISSCTVPRDVTCCGRKNQY-----PHYSENLFQFNCISLCLNG-TVHLS 117  
DB 99 SSTTDT--QVEIPATCKQNNPVCAEAGPYCALKTH--SGSCPCQMLPSVGGPGFVASS 154  
QY 118 CGEKQNTV--TCHAGFFLENECVSCNCKSKSLECKTLCLP 157  
DB 155 RAPNENVLCKACAPTF--SDTTSSTVCPHPICSLAIP 193

RESULT R  
QGVZML  
T2 protein - myxoma virus (strain Lausanne)  
C:Species: myxoma virus  
C:Date: 31-Dec-1992 #sequence\_revision 31-Dec-1992 #text\_change 18-Jun-1999  
C:Accession: A40566  
R:Upton, C.; Macen, J.L.; Schreiber, M.; McFadden, G.  
Virology 184, 370-382, 1991  
A:Title: Myxoma virus expresses a secreted protein with homology to the tumor necrosis factor  
A:Reference number: A40566; MUID:91335768; PMID:1651597  
A:Accession: A40566  
A:Molecule type: DNA  
A:Residues: 1-326 <UPT>  
A:Cross references: GB:M05181; GR:M37976; NID:3332302; PIDN AAA46612 1; PID G332310  
C:Superfamily: myxoma virus T2 protein; NGF receptor repeat homology  
C:Keywords: glycoprotein  
F:64.105/Domain: NGF receptor repeat homology <NG2>  
F:106.147/Domain: NGF receptor repeat homology <NG3>  
F:66.181,205,248/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 19.1% Score 179.5; DB 1; Length 326;  
Best Local Similarity 27.4% Pred. No. 2 3e-06;  
Matches 51; Conservative 19; Mismatches 67; Indels 49; Gaps 7;

QY 13 QNNSICTYCHKGTLYNDGPGQDTPCEGSGFTASENHLPCHLSC-SKCRKEMGQ 71  
DB 34 EKDHGCTSCPPSSVASPLC-GPGSDTVCSPCKNETFTASTNHAPACVSCRGCTGHL 91  
QY 72 VEISSCTVPRDVTCCGRKNQY-----PHYSENLFQFNCISLCLNG-TVHLS 117  
DB 92 ESQSCDTRDVPVCHSACNYCLLKGQGGPICAPFTYCPAGYGVSGHTPTGDLCTKCP 150  
QY 93 RHYWSENLFPQFNCISLCLNG-TVHLSQCFKQNTVCTCHAGFFLENECVSCNCKSKSLEC 151  
DB 151 RVTYSDAVSTSTCTCTSSSENYISVERNLVPVNDTCTTTAG----PNEVVKTSFVSVLNH 206  
QY 152 TKLCLP 157  
DB 207 TD-CBP 211

RESULT 9  
B41692  
T2 protein rabbit fibroma virus  
C:Species: rabbit fibroma virus, Shope fibroma virus  
C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 07-May-1999  
C:Accession: B41692  
R:Upton, C.; DeLange, A.M.; McFadden, G.  
Virology 160, 20-30, 1987  
A:Title: Tumorigenic poxviruses: genomic organization and DNA sequence of the telomeric  
A:Reference number: A43662; MUID:87321104; PMID 2826128  
A:Accession: B41692  
A:Status: preliminary  
A:Molecule type: DNA

A:Residues: 1-325 <UPT>  
A:Cross references: GB:M17433  
C:Superfamily: myxoma virus T2 protein; NGF receptor repeat homology  
F:64.105/Domain: NGF receptor repeat homology <NG2>  
F:106.147/Domain: NGF receptor repeat homology <NG3>

Query Match 18.0% Score 178; DB 2; Length 326;  
Best Local Similarity 29.6% Pred. No. 3e-06;  
Matches 45; Conservative 15; Mismatches 62; Indels 40; Gaps 6;

QY 13 QNNSICTYCHKGTLYNDGPGQDTPCEGSGFTASENHLPCHLSC-SKCRKEMGQ 71  
DB 34 EKDHGCTSCPPSSVASPLC-GPGSDTVCSPCKNETFTASTNHAPACVSCRGCTGHL 91  
QY 72 VEISSCTVPRDVTCCGRKNQYVHWSSENLFPQFNCISLCLNG-TVHLSQCFKQNTVCTCHAG 141  
DB 92 ESQSCDTRDVPVCHSACNYCLLKGQGGPICAPFTYCPAGYGVSGHTPTGDLCTKCP 150  
QY 132 FFLRENECVSCNCK-----SLECKTLK 155  
DB 133 YGVSGHTPAGDTECKCPHPHTYSNLSLSPTEFC 164

RESULT 10  
A26431  
Nerve growth factor receptor precursor, low affinity - rat  
N:Alternate names: NGF receptor  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
C:Accession: A26431; PH1229  
R:Radeke, M.J.; Misko, T.F.; Hsu, C.; Herzenberg, L.A.; Shooter, E.M.  
Nature 325, 593-597, 1987  
A:Title: Gene transfer and molecular cloning of the rat nerve growth factor receptor  
A:Reference number: A26431; MUID:87115859; PMID:3627580  
A:Accession: A26431  
A:Molecule type: mRNA  
A:Residues: 1-425 <RAD>  
A:Cross references: GB:X05137; NID:956755; PIDN CAA28781.1; PIDN 96766  
R:Metsis, M.; Timusk, T.; Allikmets, R.; Saarma, M.; Persson, H.  
Gene 121, 247-254, 1992  
A:Title: Regulatory elements and transcriptional regulation by testostosterone and retinoid  
A:Reference number: PH1229; MUID:93077038; PMID:1446821  
A:Accession: PH1229  
A:Molecule type: DNA  
A:Residues: 1-20 <MET>  
A:Cross references: GB:X61269  
C:Comment: This receptor is found on sensory and sympathetic neurons, on neuroblastoma cells  
C:Comment: The cysteine-rich region of the extracellular domain may form part or all of the binding site  
C:Comment: This protein is thought to form a high-affinity receptor when it associates with

A:Introns: 20/3  
C:Superfamily: nerve growth factor receptor; NGF receptor repeat homology  
C:Keywords: duplication; glycoprotein; heterodimer; monomer; phosphorylation; receptor; T2 protein  
F:1.29/Domain: signal sequence #status predicted <SIG>  
F:30-425/Product: nerve growth factor receptor #status predicted <EXT>  
F:30-251/Domain: extracellular #status predicted <EXT>  
F:33-66/Domain: NGF receptor repeat homology <NG1>  
F:68-109/Domain: NGF receptor repeat homology <NG2>  
F:110-148/Domain: NGF receptor repeat homology <NG3>  
F:150-190/Domain: NGF receptor repeat homology <NG4>  
F:198-249/Region: serine/threonine-rich  
F:252-273/Domain: transmembrane #status predicted <MEM>  
F:274-425/Domain: intracellular #status predicted <INT>  
F:61/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 18.8% Score 176.5; DB 1; Length 425;  
Best Local Similarity 30.9% Pred. No. 4 6e-06;  
Matches 50; Conservative 25; Mismatches 68; Indels 19; Gaps 10;

QY 4 QPGQYVHPPNNISICTYCHKGTLYNDGPGQDTPCEGSGFTASENHLPCHLSC 62  
DB 33 CSTGLYTH---SGECCVACNLGEGVAQPC-GANG-TVCEPCLDNVTPSDVVSATETKIC 87

Q7 123 KNTVC TCHAGFLER...EGVSGNCKSLCTCLCP 157  
 Db 142 KNTVC TCHAGFLER...EGVSGNCKSLCTCLCP 157  
 Q7 142 KNTVC TCHAGFLER...EGVSGNCKSLCTCLCP 157  
 Db 142 KNTVC TCHAGFLER...EGVSGNCKSLCTCLCP 157

## RESULT 11

148851  
 gene murine tumour necrosis factor receptor 2 (tumor necrosis factor receptor 2) (house mouse)

C.Species: Mus musculus (house mouse)  
 C.Date: 22-Oct-1999 #sequence\_revision 23-Jul-1999 #text\_change 23-Jul-1999  
 C.Accession: U49994  
 R.Powell, F. J.; Wicker, L. S.; Peterson, L. B.; Todd, J. A  
 Mamm. Genome 5: 726-727, 1994

A.Title: Alternative splicing of the type 2 tumor necrosis factor receptor gene.  
 A.Reference number: 148854, MIM:178843, PMID:7813884

A.Accession: 148854

A.Status: preliminary; translated from GB/EMBL/DBJ

A.Molecule type: mRNA

A.Residues: 1-459 <R89>

A.Cross-references: EMBL:X76901, NID:9433926, PID:9433926, PID:9433926  
 A.Superfamily: tumor necrosis factor receptor type 2, TNF receptor repeat homology  
 E111:189,190,191,192,193,194,195,196,197,198,199,200,201,202,203,204,205,206,207,208,209,210,211,212,213,214,215,216,217,218,219,220,221,222,223,224,225,226,227,228,229,230,231,232,233,234,235,236,237,238,239,240,241,242,243,244,245,246,247,248,249,250,251,252,253,254,255,256,257,258,259,260,261,262,263,264,265,266,267,268,269,270,271,272,273,274,275,276,277,278,279,280,281,282,283,284,285,286,287,288,289,290,291,292,293,294,295,296,297,298,299,300,301,302,303,304,305,306,307,308,309,310,311,312,313,314,315,316,317,318,319,320,321,322,323,324,325,326,327,328,329,330,331,332,333,334,335,336,337,338,339,340,341,342,343,344,345,346,347,348,349,350,351,352,353,354,355,356,357,358,359,360,361,362,363,364,365,366,367,368,369,370,371,372,373,374,375,376,377,378,379,380,381,382,383,384,385,386,387,388,389,390,391,392,393,394,395,396,397,398,399,400,401,402,403,404,405,406,407,408,409,410,411,412,413,414,415,416,417,418,419,420,421,422,423,424,425,426,427,428,429,430,431,432,433,434,435,436,437,438,439,440,441,442,443,444,445,446,447,448,449,450,451,452,453,454,455,456,457,458,459,460,461,462,463,464,465,466,467,468,469,470,471,472,473,474,475,476,477,478,479,480,481,482,483,484,485,486,487,488,489,490,491,492,493,494,495,496,497,498,499,500,501,502,503,504,505,506,507,508,509,510,511,512,513,514,515,516,517,518,519,520,521,522,523,524,525,526,527,528,529,530,531,532,533,534,535,536,537,538,539,540,541,542,543,544,545,546,547,548,549,550,551,552,553,554,555,556,557,558,559,560,561,562,563,564,565,566,567,568,569,570,571,572,573,574,575,576,577,578,579,580,581,582,583,584,585,586,587,588,589,590,591,592,593,594,595,596,597,598,599,600,601,602,603,604,605,606,607,608,609,610,611,612,613,614,615,616,617,618,619,620,621,622,623,624,625,626,627,628,629,630,631,632,633,634,635,636,637,638,639,640,641,642,643,644,645,646,647,648,649,650,651,652,653,654,655,656,657,658,659,660,661,662,663,664,665,666,667,668,669,670,671,672,673,674,675,676,677,678,679,680,681,682,683,684,685,686,687,688,689,690,691,692,693,694,695,696,697,698,699,700,701,702,703,704,705,706,707,708,709,710,711,712,713,714,715,716,717,718,719,720,721,722,723,724,725,726,727,728,729,730,731,732,733,734,735,736,737,738,739,740,741,742,743,744,745,746,747,748,749,750,751,752,753,754,755,756,757,758,759,760,761,762,763,764,765,766,767,768,769,770,771,772,773,774,775,776,777,778,779,780,781,782,783,784,785,786,787,788,789,790,791,792,793,794,795,796,797,798,799,800,801,802,803,804,805,806,807,808,809,810,811,812,813,814,815,816,817,818,819,820,821,822,823,824,825,826,827,828,829,830,831,832,833,834,835,836,837,838,839,840,841,842,843,844,845,846,847,848,849,850,851,852,853,854,855,856,857,858,859,860,861,862,863,864,865,866,867,868,869,870,871,872,873,874,875,876,877,878,879,880,881,882,883,884,885,886,887,888,889,890,891,892,893,894,895,896,897,898,899,900,901,902,903,904,905,906,907,908,909,910,911,912,913,914,915,916,917,918,919,920,921,922,923,924,925,926,927,928,929,930,931,932,933,934,935,936,937,938,939,940,941,942,943,944,945,946,947,948,949,950,951,952,953,954,955,956,957,958,959,960,961,962,963,964,965,966,967,968,969,970,971,972,973,974,975,976,977,978,979,980,981,982,983,984,985,986,987,988,989,990,991,992,993,994,995,996,997,998,999,1000

## Query Match

Best local similarity 18.7%, Score 176; DB 2; Length 459;  
 Matches 50; Conservative 20; Mismatches 77; Indels 14; Gaps 8;

Q7 4 CCKKYLHPQNNISICTKCHKGYLYNDGPGQDDDCRECSGSPASENHLRLHLS 63  
 Db 26 CCKKYLHPQNNISICTKCHKGYLYNDGPGQDDDCRECSGSPASENHLRLHLS 63  
 Q7 64 CCKKYLHPQNNISICTKCHKGYLYNDGPGQDDDCRECSGSPASENHLRLHLS 117  
 Db 64 CCKKYLHPQNNISICTKCHKGYLYNDGPGQDDDCRECSGSPASENHLRLHLS 117  
 Q7 82 CCKKYLHPQNNISICTKCHKGYLYNDGPGQDDDCRECSGSPASENHLRLHLS 139  
 Db 82 CCKKYLHPQNNISICTKCHKGYLYNDGPGQDDDCRECSGSPASENHLRLHLS 139  
 Q7 118 CCKKYLHPQNNISICTKCHKGYLYNDGPGQDDDCRECSGSPASENHLRLHLS 157  
 Db 118 CCKKYLHPQNNISICTKCHKGYLYNDGPGQDDDCRECSGSPASENHLRLHLS 157  
 Q7 140 CCKKYLHPQNNISICTKCHKGYLYNDGPGQDDDCRECSGSPASENHLRLHLS 178  
 Db 140 CCKKYLHPQNNISICTKCHKGYLYNDGPGQDDDCRECSGSPASENHLRLHLS 178

## RESULT 12

146476  
 B cell-associated surface molecule CD40, long splice form - mouse

C.Species: Mus musculus (house mouse)

C.Date: 12-Jun-1999 #sequence\_revision 18-Nov-1999 #text\_change 17-Nov-2000

C.Accession: A46476; A46515

R.Torres, R. M.; Clark, E. A.

J. Immunol. 146: 620-625, 1992

A.Title: Alternative splicing of an alternatively polyadenylated mRNA species of murine

A.Reference number: A46476; MIM:12105783; PMID:1370315

A.Accession: A46476

A.Status: preliminary

A.Molecule type: mRNA

A.Residues: 1-305 <TOR>

A.Cross-references: GB:M93312; NID:91553058

A.Note: Sequence extracted from NCBI database (NCBI: 75206, NCBI: 75207)

A.Note: This translation is not annotated in GenBank entry MUSCD40A, release 113.0

R.Grimaldi, J. C.; Torres, F.; Foster, C. A.; Chang, F.; Clark, E. A.; Howard, M.; Cockayne, J.

J. Immunol. 149: 3921-3926, 1992

A.Title: Structure and function of the mouse CD40 gene.

A.Reference number: A46515; MIM:12105784; PMID:1291194

A.Accession: A46515

A.Status: preliminary; not compared with conceptual translation

A.Molecule type: nucleic acid

A.Residues: 1-347 <IV> <SP>

A.Cross-references: GB:M93312, NID:91553058, PID:91553059, GB:M94126, R

A.Experimental source: BALB/c, liver

A.Note: Sequence extracted from NCBI database (NCBI: 120357)

C.Comment: For an alternative splice form, see PIR:A46476

C.Superfamily: CD27 antigen, TNF receptor repeat homology  
 C.Keywords: alternative splicing; transmembrane protein  
 F105-144/Domain: TNF receptor repeat homology <NGF>

Query Match 17.8%, Score 167.5, DB 2; Length 305;  
 Best local similarity 17.8%, Pred. No. 2.2e-05;  
 Matches 46; Conservative 23; Mismatches 72; Indels 13; Gaps 7,

Q7 4 CCKKYLHPQNNISICTKCHKGYLYNDGPGQDDDCRECSGSPASENHLRLHLS 63  
 Db 26 CCKKYLHPQNNISICTKCHKGYLYNDGPGQDDDCRECSGSPASENHLRLHLS 63  
 Q7 64 CCKKYLHPQNNISICTKCHKGYLYNDGPGQDDDCRECSGSPASENHLRLHLS 117  
 Db 64 CCKKYLHPQNNISICTKCHKGYLYNDGPGQDDDCRECSGSPASENHLRLHLS 117  
 Q7 82 CCKKYLHPQNNISICTKCHKGYLYNDGPGQDDDCRECSGSPASENHLRLHLS 139  
 Db 82 CCKKYLHPQNNISICTKCHKGYLYNDGPGQDDDCRECSGSPASENHLRLHLS 139  
 Q7 118 CCKKYLHPQNNISICTKCHKGYLYNDGPGQDDDCRECSGSPASENHLRLHLS 157  
 Db 118 CCKKYLHPQNNISICTKCHKGYLYNDGPGQDDDCRECSGSPASENHLRLHLS 157  
 Q7 140 CCKKYLHPQNNISICTKCHKGYLYNDGPGQDDDCRECSGSPASENHLRLHLS 173  
 Db 140 CCKKYLHPQNNISICTKCHKGYLYNDGPGQDDDCRECSGSPASENHLRLHLS 173

## RESULT 13

072175  
 G2R protein - variola minor virus (strain Garcia-1966)

C.Species: variola minor virus

C.Date: 24-Nov-1999 #sequence\_revision 24-Nov-1999 #text\_change 20-Jun-2000

C.Accession: U72175

R.Shelley-Krueger, S. N.; Torkelson, A. V.; Gurev, V. V.; Salzman, R. F.; Lupton, J. R.

Submitted to Genbank, March 1998

A.Description: Analysis of the complete coding sequence of DNA of alastrim variola minor

A.Reference number: A/2150

A.Accession: U72175

A.Status: preliminary

A.Molecule type: DNA

A.Residues: 1-349 <SHC>

A.Cross-references: GB:Y16780; NID:95830555; PID:95830555, PID:95830555, PID:95830555

A.Experimental source: strain Garcia-1966

C.Genetics:

A.Gene: G2R

C.Superfamily: myxoma virus T2 protein; TNF receptor repeat homology

Query Match 17.7%, Score 166.5; DB 2; Length 349;  
 Best local similarity 26.7%, Pred. No. 2.2e-05;  
 Matches 46; Conservative 19; Mismatches 64; Indels 43; Gaps 9;

Q7 4 CCKKYLHPQNNISICTKCHKGYLYNDGPGQDDDCRECSGSPASENHLRLHLS 63  
 Db 30 CCKKYLHPQNNISICTKCHKGYLYNDGPGQDDDCRECSGSPASENHLRLHLS 87  
 Q7 64 CCKKYLHPQNNISICTKCHKGYLYNDGPGQDDDCRECSGSPASENHLRLHLS 117  
 Db 64 CCKKYLHPQNNISICTKCHKGYLYNDGPGQDDDCRECSGSPASENHLRLHLS 117  
 Q7 82 CCKKYLHPQNNISICTKCHKGYLYNDGPGQDDDCRECSGSPASENHLRLHLS 131  
 Db 82 CCKKYLHPQNNISICTKCHKGYLYNDGPGQDDDCRECSGSPASENHLRLHLS 131  
 Q7 118 CCKKYLHPQNNISICTKCHKGYLYNDGPGQDDDCRECSGSPASENHLRLHLS 161  
 Db 118 CCKKYLHPQNNISICTKCHKGYLYNDGPGQDDDCRECSGSPASENHLRLHLS 161  
 Q7 132 CCKKYLHPQNNISICTKCHKGYLYNDGPGQDDDCRECSGSPASENHLRLHLS 174  
 Db 132 CCKKYLHPQNNISICTKCHKGYLYNDGPGQDDDCRECSGSPASENHLRLHLS 174

## RESULT 14

128623  
 hypothetical protein G2R - variola major virus

C.Species: variola major virus

C.Date: 22-Oct-1999 #sequence\_revision 22-Oct-1999 #text\_change 21-Jul-2000

C.Accession: U28623

F.Massey, P. F.; Esposito, J. J.; Liu, L. J.; Qi, J.; Utechtack, T. F.; Knight, J. C.; Aubin

Nature 366: 748-751, 1993

A.Title: Potential virulence determinants in terminal regions of variola smallpox virus

A.Reference number: U28623; MIM:94089747; PMID:8264798

A.Accession: U28623

A.Status: preliminary; translated from GB/EMBL/DBJ

A.Molecule type: DNA

A.Residues: 1-348 <MAS>

A:Cross references: EMBL:L22579; MID:g623595; PIDN:AAA60033.1; PID:g419102  
 A:Experimental source: strain Bangladesh 1975  
 C:Superfamily: myxoma virus T2 protein; NGF receptor repeat homology

Query Match 17 48; Score 164; DB 2; Length 348;  
 Best Local Similarity 27 88; Pred No 3 3e-05;  
 Matches 42; Conservative 17; Mismatches 54; Indels 38; Gaps 8;

QY 4 CQKRYIHPQNNISICTYTHKTYLYNCPGPGQDTDCRECSGFTASFNHLPHCLSCS 63  
 DB 11 CKDTEY---KHNLCCLSCPSTVASRLCDK-TNCTCGSGTFTSRNNHLPACLSN 86  
 QY 64 KRFEMQVEISSCTVDPDTVCGGPKNYPHYWSENLFQCF...NCSLCLNGTVHLS 117  
 DB 87 GRGNS--NQVETRSNTTHNICECPGY-----CLLKSGSGKACVST----- 130

QY 118 CQKQNTVCTCHAGFELRENECVS---CSNC 145  
 DB 131 -----KCGIGYGVSGHTSVGDVICSPC 152

RESULT 15  
 D36858  
 Gene G4R protein - variola virus  
 N:Alternate names: B2BR protein (COP)  
 C:Species: variola virus  
 C:Date: 30-Sep-1993 #sequence revision 30-Sep-1993 #text\_change 23-Mar-2001  
 C:Accession: D36858; S46888; S32385; S35987  
 R:Blinov, V.M.  
 submitted to GenBank, November 1992  
 A:Reference number: A16859  
 A:Accession: D36858  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-349 <BL>  
 A:Cross references: GB:X69198; MID:g456758; PIDN:CAA49137.1; PID:g457087  
 A:Experimental source: strain India-1967, ssp. major, isolate Ind3  
 R:Kolykhailov, A.A.; Blinov, V.M.; Gytarov, V.V.; Pozdnyakov, S.G.; Chizhikov, V.E.; Prok  
 submitted to the EMBL Data Library, April 1992  
 A:Description: Nucleotide sequence analysis of the region of Variola virus XhoI F O H P  
 A:Reference number: S46868  
 A:Accession: S46888  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-349 <KOL>  
 A:Cross references: EMBL:X67117; MID:g516428; PIDN:CAA47540.1; PID:g516449  
 A:Experimental source: strain India-1967, isolate Ind3  
 R:Shchelkunov, S.N.; Blinov, V.M.; Sandakhchiev, L.S.  
 FEBS Lett. 319, 80-83, 1993

A:Title: Genes of variola and vaccinia viruses necessary to overcome the host protective  
 A:Reference number: S32385; MID:g1262241; PID:81941.3  
 A:Accession: S32385  
 A:Molecule type: DNA  
 A:Residues: 31-168 <SHC>  
 A:Cross references: EMBL:X69198  
 A:Experimental source: strain India-1967, ssp. major

C:Genetics:  
 A:Gene: G4R  
 C:Superfamily: myxoma virus T2 protein; NGF receptor repeat homology  
 F:32 66/Domain: NGF receptor repeat homology <NGF>  
 F:68 109/Domain: NGF receptor repeat homology <NG2>  
 F:110-151/Domain: NGF receptor repeat homology <NG3>

Query Match 17 48; Score 164; DB 2; Length 348;  
 Best Local Similarity 27 88; Pred No 3 3e-05;  
 Matches 42; Conservative 17; Mismatches 54; Indels 38; Gaps 8;

QY 4 CQKRYIHPQNNISICTYTHKTYLYNCPGPGQDTDCRECSGFTASFNHLPHCLSCS 63  
 DB 11 CKDTEY---KHNLCCLSCPSTVASRLCDK-TNCTCGSGTFTSRNNHLPACLSN 87  
 QY 64 KRFEMQVEISSCTVDPDTVCGGPKNYPHYWSENLFQCF...NCSLCLNGTVHLS 117

QY 118 CQKQNTVCTCHAGFELRENECVS---CSNC 145  
 DB 131 -----KCGIGYGVSGHTSVGDVICSPC 152

QY 98 GRGNS--NQVETRSNTTHNICECPGY  
 QY 118 CQKQNTVCTCHAGFELRENECVS---CSNC 145  
 DB 132 -----KCGIGYGVSGHTSVGDVICSPC 153

Search completed: January 6, 2003, 03:59:19  
 Job time : 25 secs

QY 98 GRGNS--NQVETRSNTTHNICECPGY  
 QY 118 CQKQNTVCTCHAGFELRENECVS---CSNC 145  
 DB 132 -----KCGIGYGVSGHTSVGDVICSPC 153

Search completed: January 6, 2003, 03:59:19  
 Job time : 25 secs

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GenCore version 5.1.3  
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QM protein - protein search, using sw model

Run on: January 6, 2003, 03:46:34 ; Search time 14 Seconds  
(without alignments)

476.978 Million cell updates/sec

Title: US-09-882-735-2

Perfect score: 941

Sequence: 1 DSVCPQKQYHPQNNISCTT... CSNCFYSUECTKLCPLQIEN 161

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40:\*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	941	100.0	455	1	TR1A_HUMAN
2	716.5	76.1	461	1	TR1A_PIG
3	680	72.3	454	1	TR1A_MOUSE
4	674.5	71.7	471	1	TR1A_BOVIN
5	669	71.1	461	1	TR1A_RAT
6	200.5	21.3	176	1	TR23_MOUSE
7	200.5	21.3	417	1	TR12_HUMAN
8	198.5	21.1	180	1	TR22_MOUSE
9	187.5	19.9	435	1	TRN3_HUMAN
10	182.5	19.4	427	1	TR16_HUMAN
11	181.5	19.3	417	1	TR16_MOUSE
12	181	19.2	474	1	TR1B_MOUSE
13	178.5	19.1	326	1	V72_MXVL
14	178	18.9	325	1	V72_SFVKA
15	176.5	18.8	332	1	TRN5_PIG
16	176.5	18.8	425	1	TR16_RAT
17	167.5	17.8	249	1	TRN5_MOUSE
18	167.5	17.8	415	1	TRN3_MOUSE
19	167	17.7	269	1	TRN5_BOVIN
20	166.5	17.7	323	1	TRN5_BOVIN
21	166.5	17.7	349	1	TRN5_MOUSE
22	164	17.4	349	1	TRN5_MOUSE
23	164	17.4	351	1	TRN5_MOUSE
24	164	17.4	401	1	TR1R_HUMAN
25	162.5	17.3	327	1	TRN5_MOUSE
26	161	17.1	461	1	TR1B_HUMAN
27	158	16.8	401	1	TR1B_RAT
28	154	16.4	401	1	TR1B_MOUSE
29	147	15.6	324	1	TRN6_RAT
30	147	15.4	416	1	TR16_CHICK
31	142	15.1	283	1	TR14_HUMAN
32	142	15.1	386	1	TR10D_HUMAN
33	141	15.0	1680	1	FUR2_DROME

RESULT 1

ID	TR1A_HUMAN	STANDARD;	PRT;	455 AA.
AC	P19438;			
DT	01-FEB-1991 (Rel. 17, Created)			
DT	01-FEB-1991 (Rel. 17, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Tumor necrosis factor receptor superfamily member 1A precursor (p60)			
DE	(TNF-R1) (TNF-R1) (p55) (CD120a) [Contains: Tumor necrosis factor binding protein 1 (TNFRI)]			
GN	TNFRSF1A OR TNFR1 OR TNFAR.			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Placenta;			
RX	MEDLINE=90235285; PubMed=2158863;			
RA	Schall T.J., Lewis M., Koller K.J., Lee A., Rice G.C., Wong G.H.W., Getanaga T., Granger G.A., Lenz P., Paab H., Kohn W.J., Goodfield D.V.			
RA	"Molecular cloning and expression of the human 55 kd tumor necrosis factor receptor."			
RL	Cell 61:361-370(1990).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=90235284; PubMed=2158862;			
RA	Loetscher H., Pan Y.-C.E., Lahm H.-W., Gentz R., Brockhaus M., Tabuchi H., Lesslauer W.			
RA	"Molecular cloning and expression of the human 55 kd tumor necrosis factor receptor."			
RL	Cell 61:351-359(1990).			
RN	[3]			
RP	SEQUENCE FROM N.A. AND SEQUENCE OF 41-53, 110-124 AND 199-201.			
RX	MEDLINE=91006021; PubMed=1698610;			
RA	Nopar Y., Kemper O., Brakelusch C., Engelmann H., Zwanq R., Aderka D., Holtmann H., Wallach D.			
RA	"Soluble forms of tumor necrosis factor receptors (TNF-R). The cDNA for the type I TNF-R, cloned using amino acid sequence data of its soluble form, encodes both the cell surface and a soluble form of the receptor."			
RL	EMBO J. 9:3263-3278(1990).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=91090841; PubMed=1702293;			
RA	Himmeler A., Maurer-Foy I., Kronke M., Scheurich P., Pflanzmann K., Lantz M., Glessner I., Hauptmann R., Strataw C., Adolf G.R.			
RA	"Molecular cloning and expression of human and rat tumor necrosis factor receptor chain (p60) and its soluble derivative, tumor necrosis factor-binding protein."			
RL	DNA Cell Biol. 9:705-715(1990).			
RN	[5]			
RP	SEQUENCE FROM N.A.			
RX	TISSUE=Placenta;			
RC	TISSUE=Placenta;			
RX	MEDLINE=91017509; PubMed=2170974;			
RA	Gray P.W., Barrett K., Chantry D., Turner M., Feldman M.			

P41272 mus musculus  
P25942 homo sapien  
O14798 h tumor nec  
P26842 homo sapien  
O14763 homo sapien  
O08114 E. coli  
O04592 mus musculus  
P92127 G. gallus  
O92824 mus musculus  
O92824 mus musculus  
P47741 mus musculus  
P25445 homo sapien

CC "Cloning of human tumor necrosis factor (TNF) receptor cDNA and  
 CC expression of recombinant soluble TNF-binding protein.";  
 CC Proc Natl Acad Sci U S A. 87:7380-7384(1990).  
 CC [6]  
 CC RP SEQUENCE FROM N.A.  
 CC MEDLINE=92250049; PubMed=115171;  
 CC Fuchs F., Streibl S., Dworzak M., Himmler A., Ambros P.F.;  
 CC "Structure of the human TNF receptor 1 (p60) gene (TNFR1) and  
 CC localization to chromosome 12p13.";  
 CC Genomics 12:219-224(1992).  
 CC [7]  
 CC RP SEQUENCE FROM N.A.  
 CC TISSUE=Muscle;  
 CC Strausberg R.;  
 CC Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
 CC [8]  
 CC RP SEQUENCE OF 41-45.  
 CC MEDLINE=90110215; PubMed=2153136;  
 CC Engelmann H., Novick D., Wallach D.;  
 CC "Two tumor necrosis factor-binding proteins purified from human  
 CC urine. Evidence for immunological cross-reactivity with cell surface  
 CC tumor necrosis factor receptors.";  
 CC J. Biol. Chem. 265:1531-1536(1990).  
 CC [9]  
 CC RP X-RAY CRYSTALLOGRAPHY (2.85 ANGSTROMS) OF 30-211 IN COMPLEX WITH TNFB.  
 CC MEDLINE=93258809; PubMed=8387891;  
 CC Brierley P.W., P'Arcy A., Jones W., Schoenfeld H.-C.,  
 CC Bioger C., Loetscher H., Lesslauer W.;  
 CC "Crystal structure of the soluble human 55 kd TNF receptor-human TNF  
 CC beta complex: implications for TNF receptor activation.";  
 CC Cell 73:431-445(1993).  
 CC [10]  
 CC RP X-RAY CRYSTALLOGRAPHY (1.85 ANGSTROMS) OF 41-202.  
 CC MEDLINE=97094982; PubMed=8939750;  
 CC Nalsmith J.H., Devine T.G., Khoo H., Sprang S.R.;  
 CC "Structures of the extracellular domain of the type I tumor necrosis  
 CC factor receptor.";  
 CC Structure 4:1251-1262(1996).  
 CC [11]  
 CC RP VARIANT: TNF ASG-59, TYR-62, MET-79, PHE-81, ARG-117 AND TYR-117.  
 CC MEDLINE=94213501; PubMed=1019430;  
 CC McDermott M.F., Akentjevich I., Galon J., McDermott E.M.,  
 CC Ogunkolade B.W., Gentile M., Mansfield E., Gattin M., Karenko L.,  
 CC Peterson T., McCarthy J., Frucht D.M., Aringer M., Torosyan Y.,  
 CC Teppo A.-M., Wilson M., Karastan H.M., Man Y., Todd I., Wood G.,  
 CC Schlimmer P., Kuzajewa T.P., Cooper S.M., Vella P., Amos C.I.,  
 CC Mulley J., Quane K.A., Molloy M.G., Knaki A., Powell R.J.,  
 CC Hilman G.A., O'Shea J., Kastner D.L.;  
 CC "Germline mutations in the extracellular domains of the 55 kDa TNF  
 CC receptor, TNFR1, define a family of dominantly inherited  
 CC autoinflammatory syndromes.";  
 CC Cell 97:133-144(1999).  
 CC [12]  
 CC RP FUNCTION: Receptor for TNFSF2/TNF-alpha and homotrimeric  
 CC TNFSF1/lymphotxin-alpha. The adaptor molecule FADD recruits  
 CC caspase-8 to the activating receptor. The resulting death-inducing  
 CC signaling complex (DISC) performs caspase-8 proteolytic activation  
 CC which initiates the subsequent cascade of caspases (aspartate-  
 CC specific cysteine proteases) mediating apoptosis. Contributes to  
 CC the induction of noncytotoxic TNF effects including anti-viral  
 CC state and activation of the acid sphingomyelinase.  
 CC [13]  
 CC RP SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO  
 CC HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS  
 CC PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY  
 CC WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING  
 CC PROTEINS SUCH AS TRAF6, RIP AND POSSIBLY FADD, ARE RECRUITED TO  
 CC TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX  
 CC ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND  
 CC NF-KAPPA B SIGNALING.  
 CC [14]  
 CC RP SUBCELLULAR LOCATION: Type I membrane protein and secreted.  
 CC [15]  
 CC RP DOMAIN: THE DOMAIN THAT INDUCES A-SMASE IS PROBABLY IDENTICAL TO  
 CC NECESSARY AND SUFFICIENT FOR ACTIVATION OF N-SMASE.  
 CC [16]  
 CC RP PTM: The soluble form is produced from the membrane form by  
 CC proteolytic processing.  
 CC [17]  
 CC RP DISEASE: Defects in TNFRSF1A are a cause of autosomal dominant  
 CC familial hibernian fever (PHF), a disease characterized by  
 CC recurrent fever, abdominal pain, localized tender skin lesions and  
 CC myalgia.  
 CC [18]  
 CC RP SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.  
 CC [19]  
 CC RP SIMILARITY: CONTAINS 1 DEATH DOMAIN.  
 CC [20]  
 CC RP DATABASE: NAME=PROW; NOTE=CD guide CD120a entry;  
 CC WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd120a.htm".  
 CC [21]  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC [22]  
 CC RP EMBL; X55133; CAA39021.1; -;  
 CC EMBL; M33294; AAA03210.1; -;  
 CC EMBL; M58286; AAA36753.1; -;  
 CC EMBL; M63121; AAA36754.1; -;  
 CC EMBL; M75866; AAA61201.1; -;  
 CC EMBL; M75864; AAA61201.1; JOINED.  
 CC EMBL; M75865; AAA61201.1; JOINED.  
 CC EMBL; M60275; AAA36756.1; -;  
 CC EMBL; A21522; CAA01558.1; -;  
 CC EMBL; BC010140; AAH0140.1; -;  
 CC PIR; A34899; GQHUTL.  
 CC PIR; A35010; A35010.  
 CC PIR; S12057; S12057.  
 CC PIR; A38208; A38208.  
 CC PDB; 1TNR; 31-JUL-94.  
 CC PDB; 1NCF; 07-DEC-95.  
 CC PDB; 1EXT; 11-JAN-97.  
 CC GeneW; HGNC:11916; TNFRSF1A.  
 CC MIM; 191190; -;  
 CC MIM; 142680; -;  
 CC InterPro; IP8000488; Death.  
 CC InterPro; IP8001368; TNFR\_c6.  
 CC Pfam; PF00020; TNFR\_c6; 4.  
 CC Pfam; PF00531; death; 1.  
 CC ProDom; PD000771; TNFR\_c6; 1.  
 CC SMART; SM00005; DEATH; 1.  
 CC SMART; SM00208; TNFR; 4.  
 CC PROSITE; PS00652; TNFR\_NGFR\_1; 3.  
 CC PROSITE; PS50050; TNFR\_NGFR\_2; 3.  
 CC PROSITE; PS50017; DEATH DOMAIN; 1.  
 CC Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal;  
 CC Disease mutation; Polymorphism; 3d-structure.  
 CC SIGNAL  
 CC FT 1 455  
 CC CHAIN 22 455  
 CC FT  
 CC CHAIN 41 291  
 CC FT  
 CC DOMAIN 22 211  
 CC FT  
 CC DOMAIN 212 234  
 CC FT  
 CC DOMAIN 235 455  
 CC FT  
 CC REPEAT 43 82  
 CC FT  
 CC REPEAT 83 125  
 CC FT  
 CC REPEAT 126 166  
 CC FT  
 CC REPEAT 167 196  
 CC FT  
 CC DOMAIN 338 348  
 CC FT  
 CC DOMAIN 356 441  
 CC FT  
 CC DISULFID 44 58  
 CC FT  
 CC DISULFID 59 72  
 CC FT  
 CC DISULFID 62 81  
 CC FT  
 CC DISULFID 84 99  
 CC FT  
 CC DISULFID 102 117  
 CC FT  
 CC DISULFID 105 125  
 CC FT  
 CC DISULFID 127 143  
 CC FT  
 CC DISULFID 146 158  
 CC FT  
 CC DISULFID 149 166  
 CC FT  
 CC DISULFID 168 179  
 CC FT



Query Match 100.0%; Score 941; DR 1; Length 455;  
Best Local Similarity 100.0%; Pred. No. 1 2e-71;  
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSVTPQKYYIHQNNISGCTCTCHGKTYLYNDGPGGQGTDCRCESGSPFASENHLRHCL 60  
Db 41 DSVTPQKYYIHQNNISGCTCTCHGKTYLYNDGPGGQGTDCRCESGSPFASENHLRHCL 100

QY 61 SCSKPPFEMGQVEISSCTVNPDTVCGCPKQYHYWSENLPQCFNCSLCLNGTVHLSQCE 120  
Db 101 SCSKPPFEMGQVEISSCTVNPDTVCGCPKQYHYWSENLPQCFNCSLCLNGTVHLSQCE 160

QY 121 FQNTVCTCHAGFPFLPBNPQVSCNSCKYFSLCTKLCPLQIEN 161  
Db 161 FQNTVCTCHAGFPFLPBNPQVSCNSCKYFSLCTKLCPLQIEN 261

RESULT 2  
TRIA FIG  
ID TRIA FIG STANDARD; PRT; 461 AA.  
AC P50555;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Tumor necrosis factor receptor superfamily member 1A precursor (p60)  
DE (TNF-R1) (TNF-R1) (p55).  
CN TNFRSF1A OR TNFR1.  
OS Sus scrofa (Pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Suina, Suidae, Sus.  
OX NCBI TaxID=9823;  
RN 1  
RF SEQUENCE FROM N A  
RC MEDLINE=96011645; PubMed=7590278;  
RA Suter B., Pauli U.H.;  
RT "Cloning of the cDNA encoding the porcine p55 tumor necrosis factor receptor.";  
RL Gene 163:263-266(1995).

CC - FUNCTION: Receptor for TNFRSF2/TNF alpha and homotrimeric  
CC TNFRSF1/lymphotoxin-alpha. The adaptor molecule FADD recruits  
CC caspase-8 to the activated receptor. The resulting death-inducing  
CC signaling complex (DISC) performs caspase-8 proteolytic activation  
CC which initiates the subsequent cascade of caspases (aspartate-  
CC specific cysteine proteases) mediating apoptosis (by similarity).  
CC SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO  
CC HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS  
CC PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY  
CC WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING  
CC PROTEINS SUCH AS TRAFs, RIP AND POSSIBLY FADD, ARE RECRUITED TO  
CC TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX  
CC ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND  
CC NF-KAPPA B SIGNALING (BY SIMILARITY).  
CC - SURCELLULAR LOCATION: Type I membrane protein.  
CC - SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.  
CC - SIMILARITY: CONTAINS 1 DEATH DOMAIN.

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CC EMBL: U19994; AAC48499.1; -  
CC HSSP: P19438; 1TNR.  
CC InterPro: IPR000488; Death.  
CC InterPro: IPR001368; TNFR\_c6.  
CC Pfam: PF00020; TNFR\_c6; 3.  
CC Pfam: PF00531; death; 1  
CC Problem: PD000771; TNFR\_c6; 1.

DR SMART; SM00005; DEATH; 1.  
DP SMART; SM00208; TNFR; 3.  
DR PROSITE; PS00652; TNFR\_NGFR\_1; 3.  
DR PROSITE; PS00050; TNFR\_NGFR\_2; 2.  
DR PROSITE; PS00017; DEATH\_DOMAIN; 1.  
PW Receptor; Apoptosis; Transmembrane; glycoprotein; Repeat; Simul.  
FT SIGNAL 1 21 POTENTIAL.  
FT CHAIN 22 461 TUMOR NECROSIS FACTOR RECEPTOR  
FT DOMAIN 22 210 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 211 233 SUPERFAMILY MEMBER 1A.  
FT DOMAIN 234 461 POTENTIAL.  
FT REPEAT 43 82 CYTOPLASMIC (POTENTIAL).  
FT REPEAT 83 125 TNFR-CYS 1.  
FT REPEAT 126 166 TNFR-CYS 2.  
FT REPEAT 167 195 TNFR-CYS 3.  
FT REPEAT 196 350 TNFR-CYS 4.  
FT DOMAIN 340 350 N-SMASE ACTIVATION DOMAIN (NCSD).  
FT DOMAIN 362 447 DEATH.  
FT DISULFID 44 58 BY SIMILARITY.  
FT DISULFID 59 72 BY SIMILARITY.  
FT DISULFID 62 81 BY SIMILARITY.  
FT DISULFID 84 99 BY SIMILARITY.  
FT DISULFID 102 117 BY SIMILARITY.  
FT DISULFID 105 125 BY SIMILARITY.  
FT DISULFID 127 143 BY SIMILARITY.  
FT DISULFID 146 158 BY SIMILARITY.  
FT DISULFID 149 166 BY SIMILARITY.  
FT DISULFID 168 179 BY SIMILARITY.  
FT DISULFID 182 194 BY SIMILARITY.  
FT DISULFID 185 190 BY SIMILARITY.  
FT CARBOHYD 54 54 N-LINKED (GLNAC... ) (POTENTIAL).  
FT CARBOHYD 86 86 N-LINKED (GLNAC... ) (POTENTIAL).  
FT CARBOHYD 145 145 N-LINKED (GLNAC... ) (POTENTIAL).  
FT CARBOHYD 151 151 N-LINKED (GLNAC... ) (POTENTIAL).  
SQ SEQUENCE 461 AA; 50696 MW; CD73361E6C60C9D43 CRC64;

Query Match 76.1%; Score 716.5; DR 1; Length 461;  
Best Local Similarity 77.4%; Pred. No. 5.8e-53;  
Matches 120; Conservative 12; Mismatches 22; Indels 1; Gaps 1;

QY 1 DSVTPQKYYIHQNNISGCTCTCHGKTYLYNDGPGGQGTDCRCESGSPFASENHLRHCL 60  
Db 41 DSVTPQKYYIHQNNISGCTCTCHGKTYLYNDGPGGQGTDCRCESGSPFASENHLRHCL 100

QY 61 SCSKPPFEMGQVEISSCTVNPDTVCGCPKQYHYWSENLPQCFNCSLCLNGTVHLSQCE 120  
Db 101 SCSKPPFEMGQVEISSCTVNPDTVCGCPKQYHYWSENLPQCFNCSLCLNGTVHLSQCE 160

QY 121 FQNTVCTCHAGFPFLPBNPQVSCNSCKYFSLCTKLCPLQIEN 155  
Db 161 FQNTVCTCHAGFPFLPBNPQVSCNSCKYFSLCTKLCPLQIEN 194

RESULT 3  
TRIA MOUSE  
ID TRIA MOUSE STANDARD; PPT; 454 AA.  
AC P25118;  
DT 01-MAY-1992 (Rel. 22, Created)  
DT 01-MAY-1992 (Rel. 22, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Tumor necrosis factor receptor superfamily member 1A precursor (p60)  
DE (TNF-R1) (TNF-R1) (p55).  
CN TNFRSF1A OR TNFR1 OR TNFR-1.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI TaxID=10090;  
RN 1  
RF SEQUENCE FROM N A.  
RC MEDLINE=91187885; PubMed=1849278;  
RA Lewis M., Tartaglia L.A., Lee A., Bennett G.L., Rice G.C.,  
PA Wong G.H., Chen E.Y., Goeddel D.V.;  
RT "Cloning and expression of cDNAs for two distinct murine tumor-

PT necrosis factor receptors demonstrate one receptor is species  
RT specific." ;  
PL Proc Natl Acad Sci U S A 89:2870-2874(1991)  
RN [12]  
PP SEQUENCE FROM N.A  
RX MEDLINE=91241618, PubMed=1645445,  
RA Goodwin R.G., Anderson D., Jerry R., Davis T., Brannan C.I.,  
RJ Copeland N.G., Jenkins N.A., Smith C.A.;  
RT "Molecular cloning and expression of the type 1 and type 2 murine  
PL receptors for tumor necrosis factor." ;  
RN Mol. Cell. Biol. 11:3020-3026(1991)  
RN [13]  
PP SEQUENCE FROM N.A  
RX MEDLINE=91285014; PubMed=1647956;  
RA Barrett K., Taylor-Fishwick D.A., Cope A.P., Kissenerghis A.M.,  
RJ Gray P.W., Feldman M., Foxwell B.M.J.;  
RT "Cloning, expression and cross-linking analysis of the murine p55  
PL tumor necrosis factor receptor." ;  
RN Eur. J. Immunol. 21:1649-1656(1991)  
RN [14]  
PP SEQUENCE FROM N.A  
RX TISSUE= spleen;  
RJ MEDLINE=92039815; PubMed=1657763;  
RA Roche J.C., Brockhaus M., Gentz R., Lesslauer W.;  
RT "Molecular cloning and expression of the mouse tnfr receptor type b." ;  
RN J. Immunogenetics 34:338-340(1991)  
RN [15]  
PP SEQUENCE FROM N.A  
RX MEDLINE 94245293; PubMed 8188324,  
RJ Babo B.P., Linthicum D.S.;  
RT "Nucleotide sequence of the TNF type 2 receptor from a mouse  
PL endothelioma cell line." ;  
RN J. Immunogenetics 39:450-451(1994)  
RN [16]  
PP SEQUENCE FROM N.A.  
RX MEDLINE=93137771; PubMed=8181516;  
RA Roche J., Blüthmann H., Gentz R., Lesslauer W., Steinmetz M.;  
RT "Genetic organization and promoter function of the murine tumor  
PL necrosis factor receptor beta gene." ;  
RN Mol. Immunol. 30:165-175(1993)  
RN [17]  
PP SEQUENCE FROM N.A  
RA Strausberg R.;  
RT Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases  
RN [18]  
PL FUNCTION: Receptor for TNFSF2/TNF-alpha and homotrimeric  
RN TNFSF1/lymphotoxin-alpha. The adaptor molecule FADD recruits  
CC caspase-8 to the activated receptor. The resulting death-inducing  
CC signaling complex (DISC) performs caspase-8 proteolytic activation  
CC which initiates the subsequent cascade of caspases (aspartate-  
CC specific cysteine proteases) mediating apoptosis (by similarity).  
CC -1- SUBUNIT: THE BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO  
CC HOMOPOLYMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS  
CC PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY  
CC WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING  
CC PROTEINS SUCH AS TRAFs, RIP AND POSSIBLY FADD, ARE RECRUITED TO  
CC TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX  
CC ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND  
CC NF KAPPA B SIGNALING (BY SIMILARITY).  
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -1- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.  
CC -1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.  
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CC -----  
DR EMBL: M60468; AAA39751.1; -  
DR EMBL: M59377; AAA40464.1; -  
DR EMBL: X59248; CAA41922.1; -

DR	EMBL; X57796; CAA0936.1; -
DR	EMBL; L26349; AAA5936.1; -
DR	EMBL; M76545; AAA4045.1; -
DR	EMBL; M88067; AAA4045.1; JOINED.
DR	EMBL; M76655; AAA4045.1; JOINED.
DR	EMBL; BC004593; AAH04593.1; -
DR	PIR; A38634; GOMSTL.
DR	PIR; S16677; S16677.
DR	PIR; S19021; S19021.
DR	HSPD; P19438; 1EXT.
DR	MGD; MG11314884; Infstfla.
DR	InterPro; IPR000488; Death.
DR	InterPro; IPR001368; TNFR_c6.
DR	Pfam; PF00020; TNFR_c6; 4.
DR	Pfam; PF00531; death; 1.
DR	ProDom; PD000771; TNFR_C6; 1.
DR	SMART; SM00005; DEATH_1.
DR	SMART; SM00208; TNFR; 3.
DR	PROSITE; PS00652; TNFR_NGFR_1; 3.
DR	PROSITE; PS50050; TNFR_NGFR_2; 3.
DR	PROSITE; PS50017; DEATH_DOMAIN_1.
KW	Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.
FT	SIGNAL
FT	CHAIN
FT	DOMAIN
FT	TRANSMEM
FT	DOMAIN
FT	REPEAT
FT	REPEAT
FT	REPEAT
FT	REPEAT
FT	DOMAIN
FT	DISULFID
FT	DISULFID
FT	DISULFID
FT	DISULFID
FT	DISULFID
FT	DISULFID
FT	DISULFID
FT	DISULFID
FT	DISULFID
FT	CARBOHYD
FT	CARBOHYD
FT	CARBOHYD
FT	CONFLICT
SU	SEQUENCE
Query Match	Best Local Similarity
Matches 112;	Conservative 19; Mismatches 26; Indels 0; Gaps 0;
Cy	1 DSVGPQKYLHPNNISICTCKKHKGTYLYNCPRGQDTORCEESSPTASNHRLCL 60
Lb	41 DSLCPQKLVHSSNNISICTCKKHGTLYVSDCPSPGRVTVCBEKEKSTPTASNYLRGL 100
Cy	61 SCSCKRERMQVEIISCTVDRTVGCGRKNQYRHWSENLFQCNCSLCINGTVHSCE 120
Lb	101 SCTCKREMSQVEIISPQADKDTVCGCCENGFQRYLSFTHTQCVLDVCSPCNGIVITLPCKE 160
Cy	121 KONTVCTCHAGFLIRENECVSCSNCKSLECTKLCLP 157
Lb	161 TONTVNCHAGFLIRSEECVPSHCCKNEBCKMLCLP 197
RESULT 4	
ID TRIA_BOVIN	STANDARD; PRT; 471 AA.
AC 019131;	







DR	EMBL:	U83599;	AAB41434.1;	-
DR	EMBL:	U83600;	AAB41435.1;	-
DR	EMBL:	U76029;	AAB40916.1;	-
DR	EMBL:	U74611;	AAB39714.1;	-
DR	EMBL:	U94501;	AACG1306.1;	-
DR	EMBL:	U94504;	AACG1309.1;	-
DR	EMBL:	U94502;	AACG1307.1;	-
DR	EMBL:	U94503;	AACG1308.1;	-
DR	EMBL:	U94505;	AACG1310.1;	-
DR	EMBL:	U94506;	AACG1311.1;	-
DR	EMBL:	U94508;	AACG1313.1;	-
DR	EMBL:	U94509;	AACG1314.1;	-
DR	EMBL:	U94510;	AACG1315.1;	-
DR	EMBL:	U94512;	AACG1316.1;	-
DR	EMBL:	U93598;	AAB41433.1;	-
DR	EMBL:	AF026070;	AAC39556.1;	-
DR	EMBL:	AF026071;	AAB62268.1;	-
DR	EMBL:	AB051850;	BAB40622.1;	-
DR	EMBL:	AB051851;	BAB40633.1;	-
DR	EMBL:	U75382;	AACG1192.1;	-
DR	EMBL:	U75381;	AACG1193.1;	-
DR	EMBL:	U83597;	AAB41432.1;	-
DR	GenBank:	H0NC11910;	TNFRSF12.	-
DR	MIM:	603866;	-	-
DR	Interpro:	IPI000484;	Death	-
DR	Interpro:	IP000359;	TNFR_c6.	-
DR	Interpro:	IP000359;	TNFR_c6; 2.	-
DR	Pfam:	PF00531;	death_1.	-
DR	Protein:	IP000484;	TNFR_His_1; 2.	-
DR	Protein:	P58007;	TNFR_NPR2; 1.	-
DR	Protein:	P58007;	DEATH_DOMAIN; 1.	-
RW	Pro-prog:	Amiprogst;	transmembrane; Alternative splicing; Signal;	-
RW	Repeat:	Polymorphism.	-	-
KM	SIGNAL	1	24	-
FT	CHAIN	25	417	-
FT	DOMAIN	25	199	-
FT	TRANSMEM	200	200	-
FT	DOMAIN	223	417	-
FT	REPEAT	34	71	-
FT	REPEAT	72	115	-
FT	REPEAT	116	163	-
FT	REPEAT	154	132	-
FT	REPEAT	332	413	-
FT	DISEPID	35	47	-
FT	DISEPID	48	61	-
FT	DISEPID	51	70	-
FT	DISEPID	73	89	-
FT	DISEPID	92	107	-
FT	DISEPID	95	115	-
FT	DISEPID	117	130	-
FT	DISEPID	138	155	-
FT	DISEPID	141	162	-
FT	DISEPID	165	176	-
FT	DISEPID	179	191	-
FT	DISEPID	187	195	-
FT	CARCDYD	67	47	-
FT	CARCDYD	100	104	-
FT	VARSPLIC	54	98	-
FT	VARSPLIC	54	236	-
FT	VARSPLIC	156	171	-
FT	VARSPLIC	172	417	-
FT	VARSPLIC	182	200	-
FT	VARSPLIC	182	218	-
FT	VARSPLIC	219	417	-
FT	VARSPLIC	192	277	-

[illegible]

RA Suzuki H., Toyooka K., Wang K H., Weitz C., Whitaker C., Wilming L.,  
RA Hayashizaki Y., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,  
RA "Functional annotation of a full-length mouse cDNA collection.";  
RL Nature 409:685-690(2001).  
CC - SUBCELLULAR LOCATION: Type II membrane protein (Potential).  
CC - TISSUE SPECIFICITY: Ubiquitous.  
CC - SIMILARITY: CONTAINS 3 TNFR-CYS REPEATS.  
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CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/  
CC or send an email to license@isb-sib.ch)  
DR EMBL; AJ278265; CAC16406.1;  
DR EMBL; AJ276505; CAC27353.1;  
DR EMBL; AY046551; AAL05073.1;  
DR EMBL; AK012838; BAB28502.1;  
DR HSP; P19438; 1EXT.  
DR MGD; MGI:1930270; Tofrsf22.  
DR InterPro; IPR001368; TNFR\_C6.  
DR Pfam; PF00020; TNFR\_C6; 3.  
DR SMART; SM00208; TNFR; 3.  
DR PROSITE; PS00652; TNFR\_NGFR\_1; FALSE\_NEG.  
DR PROSITE; PS00650; TNFR\_NGFR\_2.  
KW Receptor; Signal anchor; Transmembrane; Glycoprotein; Repeat  
FT DOMAIN 1 20 CYTOPLASMIC (POTENTIAL); Repeat  
FT TRANSMEM 21 41 SIGNAL-ANCHOR (TYPE II MEMBRANE PROTEIN)  
FT (POTENTIAL)  
FT DOMAIN 42 180 EXTRACELLULAR (POTENTIAL)  
FT REPEAT 47 82 TNFR-CYS 1.  
FT REPEAT 84 124 TNFR-CYS 2.  
FT REPEAT 125 165 TNFR-CYS 3.  
FT DISULFID 48 59 BY SIMILARITY  
FT DISULFID 60 73 BY SIMILARITY.  
FT DISULFID 63 82 BY SIMILARITY.  
FT DISULFID 85 100 BY SIMILARITY  
FT DISULFID 103 116 BY SIMILARITY.  
FT DISULFID 126 141 BY SIMILARITY.  
FT DISULFID 144 157 BY SIMILARITY.  
FT DISULFID 147 165 BY SIMILARITY.  
FT CARBOHYD 62 62 N-LINKED (GLCNAC...) (POTENTIAL).  
FT CARBOHYD 158 158 N-LINKED (GLCNAC...) (POTENTIAL).  
FT CONFLICT 12 12 L -> V (IN REF. 3).  
FT CONFLICT 171 180 RRSASVAVPI -> NPNRLFLLL (IN REF. 2).  
SQ SEQUENCE 180 AA; 20226 MW; 4566165A054FA CRC64;  
Query Match  
Best Local Similarity 21.1%; Score 198.5; DB 1; Length 180;  
Matches 41; Conservative 18; Mismatches 59; Indels 7; Gaps 4;  
QY 4 CPQGHVHPDNNISICTVCHGVTVLYNDGPGQDTCPECSGSPFASENHLHCLSCS 63  
DB 48 CPAGEY...WSKDVCKKCSACTFWAPCE:PHTQGGQYCHGTFETKPNYLDACILCS 104  
QY 64 KPEFEMGVFISSCVDRPTVGGPFPNVPYHWSENLFGQFNCSCLNG TVHLSQCEKQ 122  
DB 105 TQKED--GEMVADSATSPPGQCTSLY-YDPPFPESCPCTYCPGGIFVLQCNSTA 161  
QY 123 NTVCN 127  
DB 162 NTVCS 166  
RESULT 9  
TNFR3 HUMAN  
ID TNR3 HUMAN STANDARD; PRT; 435 AA.  
AC P36041;  
DT 01-JUN 1994 (Rel. 29, Created)

DT 01-JUN-1994 (Rel. 29, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Tumor necrosis factor receptor superfamily member 3 precursor  
DE (Lymphotoxin-beta receptor) (Tumor necrosis factor receptor 2 related  
DE protein) (Tumor necrosis factor C receptor).  
GN LTBEP OP TNFRSF3 OP TNFCP  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
OX (1)  
RN SEQUENCE FROM N.A.  
RP TISSUE=Liver;  
RX MEDLINE=93252381; PubMed=8486360;  
PA Racus M., Chaffanet M., Cassiman J.J., den Berghe H., Marynen P.,  
RT "Construction and evaluation of a hncRNA library of human l2p  
RT transcribed sequences derived from a somatic cell hybrid.";  
RL Genomics 16:214-218(1993).  
RN (2)  
RN SEQUENCE FROM N.A.  
RP TISSUE=Lung;  
RA Strausberg R.;  
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.  
RN (3)  
PP FUNCTION  
PX MEDLINE=94225209; PubMed=8171323;  
RA Crowe P.D., van Arsdale T.L., Walter B.N., Ware C.F., Hession C.,  
FA Ehrenfels B., Browning J.L., Din W.S., Goodwin R.G., Smith C.A.,  
RT "A lymphotoxin-beta-specific receptor.";  
RL Science 264:707-710(1994).  
RN (4)  
RN CHARACTERIZATION  
PX MEDLINE=99221511; PubMed=10207006;  
RA Wu M.-Y., Wang P.-Y., Han S.-H., Hsieh S.-L.;  
RT "The cytoplasmic domain of the lymphotoxin beta receptor mediates cell  
RL death in HeLa cells.";  
RN J. Biol. Chem. 274:11868-11872(1999).  
RN (5)  
RN FUNCTION.  
PX MEDLINE=20261554; PubMed=10799510;  
RA Poorey I.A., Butrovich K.D., Glass A.A., Borboroglu S., Benedict C.A.,  
RA Whitbeck J.C., Cohen G.H., Eisenberg R.J., Ware C.F.;  
RT "The lymphotoxin-beta receptor is necessary and sufficient for  
RT LIGHT-mediated apoptosis of tumor cells.";  
RL J. Biol. Chem. 275:14307-14315(2000).  
CC - FUNCTION: Receptor for the heterotrimeric lymphotoxin containing  
CC LTA and LTb, and for TNFSF14/LIGHT. Promotes apoptosis via TRAF3  
CC and TRAF5. May play a role in the development of lymphoid organs.  
CC - SUBUNIT: Self-associates.  
CC - SUBCELLULAR LOCATION: Type I membrane protein.  
CC - SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.  
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CC or send an email to license@isb-sib.ch)  
CC EMBL; L04270; AAA36757.1;  
CC EMBL; BC026562; AAH26562.1;  
CC HSP; P25942; ICDF.  
CC Genew; HGNC:6718; LTBR.  
CC MIN; 600979;  
CC InterPro; IPR001368; TNFR\_C6.  
CC Pfam; PF00020; TNFR\_C6; 4.  
CC ProDom; PD000771; TNFR\_C6; 1.  
CC SMART; SM00208; TNFR; 4.  
CC PROSITE; PS00652; TNFR\_NGFR\_1; 2.  
CC PROSITE; PS00650; TNFR\_NGFR\_2; 3.  
KW Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal  
FT SIGNAL 1 30 POTENTIAL.









```
Matches 51; Conservative 19; Mismatches 67; Indels 49; Gaps 7,
OY 13 QNNSICCTCKCHKGTLYNDQPCRGQDQPCPCESGSPFTASENHLPHGLSC-SKCPKEMGO 71
DB 34 EKDGUCCTSCPPGASVSLC-GPGSDTVCSCKNETFTASTNHAPACVCRGRTGHLS- 91
OY 72 VEISSCTVDPTVCSCNKNQY-----
DB 92 ESQPCDTRPVPCASAGNQLLQDEGTCICAPPTKCPAGVSGHTPTGDLCTKCP 150
OY 93 RHYWENLPCFNCSLCLNG-TVHLSCEKQNTVCTCHAGFFLBENEVCVSCNCKSLEC 151
DB 151 RVTYSDAVSSTETCTSSFNYSIVFNLYPVNDTCTTAG----PNEWKTSEFSVLNH 206
OY 152 TELCLP 157
DB 207 TD CDP 211
RESULT 14
VT2 SFVKA STANDARD; PRT; 325 AA.
AC P25943;
DT 01-MAY-1992 (Rel. 22, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DE Tumor necrosis factor soluble receptor precursor (Protein T2)
GN T2.
OS Shope fibroma virus (strain Kasza) (SFV).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Leporipoxvirus
OX NCBI_TaxID=10272;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-87321103; PubMed=2820128;
RA Upton C., Delange A.M., McPadden G.;
RT "Tumor necrosis factor soluble receptor precursor: genomic organization and DNA sequence of the
telomeric region of the Shope fibroma virus genome";
RL Virology 160:20-30(1987).
RN [2]
RP FUNCTION.
RX MEDLINE-91207415; PubMed=1850261;
RA Smith C.A., Davis T., Wignall J.M., Din W.S., Farrah T., Upton C.,
RA McPadden G., Goodwin P.G.;
RT "2D open reading frame from the Shope fibroma virus encodes a soluble
form of the TNF receptor.";
RL Biochem. Biophys. Res. Commun. 176:335-342(1991)
CC -!- FUNCTION: BINDS TO TNF-ALPHA AND BETA. PROBABLY PREVENTS TNF TO
REACH CELLULAR TARGET AND THEREBY DEAMPENING THE POTENTIAL
ANTIVIRAL EFFECTS OF THE CYTOKINE.
CC -!- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
CC
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CC
CC EMBL; M17433; -; NOT ANNOTATED_CDS.
DR EMBL; A21727; CAA01687.1; -;
DR PIR; R43692; R43692.
DR HSSP; P19438; 1EXT.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 2.
DR ProDom; PD000771; TNFR_c6; 1.
DR SMART; SM00208; TNFR; 1.
DR PROSITE; PS006452; TNFR_NGFR_1, 2.
DR PROSITE; PS006450; TNFR_NGFR_2; 1.
KW Receptor; Glycoprotein; Repeat; Signal.
FT SIGNAL 1 16 POTENTIAL.
FT CHAIN 17 325 TUMOR NECROSIS FACTOR SOLUBLE RECEPTOR
```

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FT REPEAT 27 62 TNFR-CYS 1.
FT REPEAT 63 104 TNFR-CYS 2.
FT REPEAT 105 147 TNFR-CYS 3.
FT REPEAT 148 186 TNFR-CYS 4.
FT DISULFID 28 39 BY SIMILARITY.
FT DISULFID 40 53 BY SIMILARITY.
FT DISULFID 43 61 BY SIMILARITY.
FT DISULFID 64 79 BY SIMILARITY.
FT DISULFID 82 96 BY SIMILARITY.
FT DISULFID 86 104 BY SIMILARITY.
FT DISULFID 106 120 BY SIMILARITY.
FT DISULFID 123 146 BY SIMILARITY.
FT DISULFID 129 149 BY SIMILARITY.
FT DISULFID 164 185 BY SIMILARITY.
FT CARBOHYD 105 105 N-LINKED (GLCNAC...) (POTENTIAL)
FT CARBOHYD 181 181 N-LINKED (GLCNAC...) (POTENTIAL)
FT CARBOHYD 205 205 N-LINKED (GLCNAC...) (POTENTIAL)
FT CARBOHYD 238 238 N-LINKED (GLCNAC...) (POTENTIAL)
SQ SEQUENCE 325 AA; 810330339198A71E CRC64;
Query Match 18.9%; Score 178; DB 1; Length 326;
Best Local Similarity 29.6%; Prev No 30-08;
Matches 45; Conservative 15; Mismatches 62; Indels 40; Gaps 6;
OY 13 QNNSICCTCKCHKGTLYNDQPCRGQDQPCPCESGSPFTASENHLPHGLSC-SKCPKEMGO 71
DB 34 EKDGUCCTSCPPGASVSLC-GPGSDTVCSCKNETFTASTNHAPACVCRGRTGHLS 91
OY 72 VEISSCTVDPTVCSCNKNQYRHWENLPCFNCSLCLNGTCTCHAGFFLBENEVCVSCNCKSLEC 151
DB 92 ESQPCDTRPVPCASAGNQLLQDEGTCICAPPTKCPAGVSGHTPTGDLCTKCP 150
OY 132 PFLPENEVCVSCNCKY-----SLECTYIC 155
DB 133 YGVSGHTRAGDTLCEKCPHTYSDLSPTERC 164
RESULT 15
TNFR6_PIG STANDARD; PRT; 332 AA.
ID -TNR6_PIG
AC O77736;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 6 precursor (FASL
receptor) (Apoptosis-mediating surface antigen FAS) (Apo-1 antigen)
(CD95).
GN TNFRSF6 OP APT1 OP FAS
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Batling B., Hoffmann J., Holtz J., Schulz R., Heusch G., Baumer D.;
RT "Expression of apoptosis-associated genes in hibernating and stunned
myocardium of pig";
PL Submitted (JAN-1998) to the EMBL/GenBank/DDRJ databases.
CC -!- FUNCTION: Receptor for TNFSF6/FASL. The adaptor molecule FADD
recruits caspase-8 to the activated receptor. The resulting death
inducing signaling complex (DISC) performs caspase 8 proteolytic
activation which initiates the subsequent cascade of caspases
(caspase-specific cysteine proteases) mediating apoptosis. FAS
mediated apoptosis may have a role in the induction of peripheral
tolerance, in the antigen-stimulated suicide of mature T cells, or
both (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF FADD,
AND MAYBE TO OTHER CYTOSOLIC ADAPTOR PROTEINS.
CC -!- SIMILARITY: CONTAINS 3 TNFR-CYS REPEATS.
CC -!- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
CC
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QM protein protein search, using sw model  
Run on: January 6, 2003, 03:47:44 ; Search time 28 Seconds  
(without alignments)  
1184 771 Million cell updates/sec

Title: US-09-882-735-2  
Perfect score: 941  
Sequence: 1 PSVCPQKYIHPPNNSICCT.....CSNCKFFSLPCTKLCPLQIEN 161

Scoring table: BLOSUM62  
Gapop 10 0, Gapext 0 5

Searched: 671580 seqs, 206047115 residues  
Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0  
Maximum DB seq length: 200000000  
Post processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Data base : SPTRMBL 21:  
1: sp\_archaea:  
2: sp\_bacteria:  
3: sp\_fungi:  
4: sp\_human:  
5: sp\_invertebrate:  
6: sp\_mammal:  
7: sp\_mhc:  
8: sp\_organelle:  
9: sp\_phage:  
10: sp\_plant:  
11: sp\_rodent:  
12: sp\_virus:  
13: sp\_vertebrate:  
14: sp\_unclassified:  
15: sp\_rivirus:  
16: sp\_bacterioph:  
17: sp\_archaeap:  
18: sp\_mycetozoa:  
19: sp\_mollusk:  
20: sp\_invertebrate:  
21: sp\_mollusk:  
22: sp\_mollusk:  
23: sp\_mollusk:  
24: sp\_mollusk:  
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43: sp\_mollusk:  
44: sp\_mollusk:  
45: sp\_mollusk:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DR	ID	Description
1	780	82.9	446	6	Q95ND3	Q95nd3 felis silve
2	756	80.3	189	6	Q97530	Q97530 canis famil
3	731	77.7	189	6	Q95185	Q95185 felis silve
4	202	21.5	413	11	Q95MM1	Q95mm1 mus musculu
5	193	20.5	387	13	Q95VD4	Q95vd4 xenopus lae
6	191	20.3	433	11	Q912M6	Q912m6 rattus norv
7	188	20.0	302	13	Q9PUS0	Q9pus0 gallus gall
8	182.5	19.4	285	13	Q9DGH7	Q9dgh7 gallus gall
9	179.5	19.1	357	13	Q9HF34	Q9hf34 brachydanio
10	176.5	18.8	320	12	Q57079	Q57079 cowpox viru
11	176	18.7	459	11	Q62327	Q62327 mus musculu
12	175.5	18.7	312	13	Q9DGH8	Q9dgh8 gallus gall
13	175.5	18.7	322	12	Q72761	Q72761 cowpox viru
14	171.5	18.2	316	12	Q57092	Q57092 ectromelia
15	171.5	18.2	320	12	Q57091	Q57091 ectromelia
16	171.5	18.2	320	12	Q57300	Q57300 ectromelia

17	171.5	18.2	482	11	Q88734	Q88734 mus musculu
18	169	18.0	326	12	Q57120	Q57120 cowpox viru
19	168	17.9	347	12	Q57119	Q57119 cowpox viru
20	168	17.9	351	12	Q57121	Q57121 cowpox viru
21	167.5	17.8	349	12	Q57100	Q57100 cowpox viru
22	167	17.7	326	12	Q57122	Q57122 cowpox viru
23	167	17.7	347	12	Q57115	Q57115 cowpox viru
24	166.5	17.7	349	12	Q57098	Q57098 cowpox viru
25	166.5	17.7	349	12	Q57111	Q57111 cowpox viru
26	166.5	17.7	349	12	Q8UYA7	Q8uya7 cowpox viru
27	166.5	17.7	349	12	Q89098	Q89098 cowpox viru
28	166.5	17.7	349	12	Q57284	Q57284 cowpox viru
29	166	17.6	360	12	Q57118	Q57118 cowpox viru
30	165	17.5	377	6	Q8RWQ2	Q8rww2 cowpox viru
31	165	17.5	349	12	Q57109	Q57109 cowpox viru
32	164.5	17.5	348	12	Q57103	Q57103 cowpox viru
33	164.5	17.5	348	12	Q57104	Q57104 cowpox viru
34	164.5	17.5	348	12	Q57277	Q57277 cowpox viru
35	164	17.4	348	12	Q57112	Q57112 cowpox viru
36	164	17.4	348	12	Q85407	Q85407 cowpox viru
37	164	17.4	349	12	Q57110	Q57110 cowpox viru
38	164	17.4	349	12	Q89118	Q89118 cowpox viru
39	164	17.4	351	12	Q73559	Q73559 cowpox viru
40	162.5	17.3	349	12	Q57090	Q57090 cowpox viru
41	162.5	17.3	349	12	Q57101	Q57101 cowpox viru
42	162.5	17.3	349	12	Q57102	Q57102 cowpox viru
43	162.5	17.3	349	12	Q57291	Q57291 cowpox viru
44	162	17.2	349	12	Q57305	Q57305 cowpox viru
45	162	17.2	350	12	Q57123	Q57123 cowpox viru

## ALIGNMENTS

### RESULT 1

Q95ND3 ID Q95ND3 PRELIMINARY; PRT: 446 AA.  
AC Q95ND3;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
DE Tumor necrosis factor type I.  
GN TNFR I.  
OS Felis silvestris catus (Cat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.  
OX NCBI\_TaxID=9685;  
RN [1]  
RP SEQUENCE FROM N.A.  
PA Mizuno T., Goto Y., Baba K., Masuda K., Ohno K., Tsujimoto H.;  
RT "Molecular cloning of feline tumor necrosis factor receptor type I  
(TNFR I) and expression of TNFR I and TNFR II in various disease in  
cats.";  
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AB051103; BAB55455.1; ...  
DR InterPro; IPR000345; Cyt\_heme\_bind.  
DR InterPro; IPR000488; Death.  
DR InterPro; IPR000561; EGF-like.  
DR Pfam; PF00531; death; 1...  
DR Pfam; PF00020; TNFR\_c6; 4.  
DR SMART; SM00181; EGF\_1.  
DR PROSITE; PS00150; CYTOCHROME C; UNPROWN\_1.  
DR PROSITE; PS00017; DEATH\_DOMAIN; 1.  
DR PROSITE; PS01186; EGF\_2; UNKNOWN\_1.  
DR PROSITE; PS09652; TNFR\_NGFP\_1; UNPROWN\_3.  
DR PROSITE; PS00050; TNFR\_NGFP\_2; 3.  
SQ SEQUENCE 446 AA, 49563 MW, 2178D331DD8A74AA CRC64;

Query Match 82.9%; Score 780; DR 6; Length 446;  
Best Local Similarity 84.1%; Pred. No. 1,56-78;  
Matches 133; Conservative 10; Mismatches 15; Gaps 0;

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01      CTTCTTATGTCAGCCTGGCCATTGTACDPPCGTGCTGCCTCSSTFSEKTHLPHACTS   63
Db       44 CTCTAATCATGCACTGTRHAKTYTLNLTAAAGGLITLLFEENGFASMYLPQCLSCS    103
Cy       44 TCTTAATAAGGFLLENLCVSSGNCKSLAEETRLCPQLR   160
Db       104 KCFREMGVEISFTYVRRTVGDPSPNYPRYSSETHFGQCINCSICLINGTVQISCKETON 163
Cy       124 TVCTCHAGFFLRSGNELVSIVNCHEMTEIKLVVPIVE   200
Db       164 TVCTCHAGFFLRSGNELVSIVNCHEMTEIKLVVPIVE   200

RESULT 2
ID          Q97530                PRELIMINARY;               PPT;        189 AA.
AC         Q97530;
DT     01-MAY-1999 (TrEMBLrel_10, Created)
DT     01-MAY-1999 (TrEMBLrel_10, Last sequence update)
DT     01-JUN-2002 (TrEMBLrel_21, Last annotation update)
DE     Tumor necrosis factor receptor p60 (fragment).
OS     Canis familiaris (Dog).
OC     Eukaryotes, Metazoa, Chordata, Craniata, Vertebrata, Euarchontomi;
MC     Mammalia, Furbertia, Carnivora, Fissipedia; Canidae; Canis.
OX     NCBI TaxID=9615;
RN     (1)
RP     SEQUENCE FROM N.A.
RC     TISSUE=BRAIN.
RX     MEDLINE:01090932, PubMed:1182158;
RA     Campbell S.E., Nasir L., Argyle D.J., Gault E.A., Duthe S.,
RT     "Cloning of canine IL-1ra, TNFR and TIMP-2."?
RF     J Immunol 1999 Oct 1; 163(7):2214(2001);
DR     HMBL; AF013955; AAD01516.1; ?
DR     HSBB; PI4938; ITNR.
DR     InterPro; IPR000561; EGF-like.
DR     InterPro; IPR001368; TNFR_cel.
DR     Pfam; PF00020; TNFR_cof; 3.
DF     SMART; SM00708; TNFP; 3.
DL     PROSITE; PS01186; EGF_4; UNKNOWN_1.
DL     PROSITE; PS00652; TNFR_NGRF_1; 3.
LF     Prosite; TNFR_TNFR_2; 2
KW     Receptor .
SQ     NONTER.           189
SI     SEQUENCE      189 AA; 21324 MW; 5D3ADA5676FB99 CRC64;

Query Match              80.3%; Score 756; DB 6; Length 189;
Best Local Similarity    87.0%; Pred. No. 3e-76;
Matches 127; Conservative 9; Mismatches 10; Indels 0; Gaps 0

Cy       3 VEEEXYLHHGNSIGCYTKHKRYTIYNNGTFPGDDTCCEECESGSTASENHILRHLSG   62
Db       43 LCPEPKXIHLDSDSIDCTRKHKTLYLNDCPPGLDIIDCREENGCTFASENHLROCLSC   102
Cy       43 SPCTEFWZJWEISSTVDVTVCPCPFNDYRRHWSENIPCFENSCLINGTVHSICOEQ   122
Db       103 SKCKEKMNQVEISPCTYVRTGVGCCRKNOYRWSETIFQQNNCSICLINGTVISCOEQ   162
Cy       123 NTVCTCHAFFLENECVSSSNCKKS   148
Db       163 NTICTHAAGFFLRHCVCNVCKKK   188

RESULT 3
ID          Q95185                PRELIMINARY;               PPT;        189 AA.
AC         Q95185;
DT     01-FEB-1997 (TrEMBLrel_02, Created)
DT     01-JUN-1998 (TrEMBLrel_06, Last sequence update)
DT     01-JUN-2002 (TrEMBLrel_21, Last annotation update)
DE     Tumour necrosis factor receptor p60 (Fragment).
DS     Felis silvestris catus (Cat).
```

CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
CX	NCBI_TaxID=9685;
RN	(1)
RP	SEQUENCE FROM N.A.
RA	Duthie S., Nasir L., Eckersall P.D.;
RT	"Felis catus tumour necrosis factor receptor p60 (TNFR-1) mRNA,
RL	partial cds.";
DR	Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
DR	EMBL; U72344; AAB95089.1; -.
DR	HSSP; P19438; TEXT.
DR	InterPro; IPR000561; EGF-like.
DR	InterPro; IPR001368; TNFR_c6.
DR	Pfam; PF00020; TNFR_c6; 3.
DR	SMART; SM00208; TNFR_3.
DR	PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR	PROSITE; PS00652; TNFR_NGFR_1; 3.
DK	Receptor; PSS0050; TNFR_NGFR_2; 3.
KW	Receptor.
FT	NON TER
SO	SEQUENCE 189 AA; 21420 MW; F3FBDCB809D7DBE CRC64;
Query Match	77.7%; Score 731; DB 6; Length 189;
Best Local Similarity	85.5%; Pred. No. 1.8e-73;
Matches 124; Conservative	8; Mismatches 13; Indels 0; Gaps 0;
Oy	4 CPQKGIHPNNNSICCTCKHKGSTLYVNDPCPGQDTDCRECSGSFPASENHLRHLCIS 63      ::   :: :     : : :
Db	44 CPOKGIHPDNDSICTCKHKGTIYLNDCEBGDLTDCREENGTFFASNIYLRQLSLS 103      ::   :: :     : : :
Oy	64 KCRKMGQVEISSCTVDRTVCGRCKRQYRWSENLPQCNGSLCINGTVHLSCGEKN 123      ::   :: :     : : :
Db	104 KCFKEMYGVIEISPTRYRDTCGRKRQYRWSETHFCINCLSLCINTVQISCRETOR 163      ::   :: :     : : :
Oy	124 TVCTCHAGFLRENECVSCSNCKKS 148      ::   :: :     : : :
Db	164 TVCTCHAGFLRNECVSCVNCKKN 188      ::   :: :     : : :
RESULT 4	
O39MM1	13 IFELIMINAFY; FRT, 413 AA.
AC	099MM1;
DT	01-JUN-2001 (TEMBLrel. 17, Created)
DT	01-JUN-2001 (TEMBLrel. 17, Last sequence update)
DT	01-JUN-2002 (TEMBLrel. 21, Last annotation update)
DE	WSL-1-like protein.
CN	TNFRSF12.
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX	NCBI_TaxID=10090;
RN	[1]
RP	SEQUENCE FROM N.A.
RA	STEPAINE-129/SV;
RX	MEDLINE=21158384; PubMed=11261933;
RA	Wang E.C.Y., Klison J., Thern A., Williamson J., Farrow S.N.,
RT	Owen M.D.;
RT	"genomic structure, expression, and chromosome mapping of the mouse
RT	homolog for the WSL-1 (DR3, Apo3, TRAMP, LARD, TR3, TNFRSF12)
RT	gene.";
RL	Immunogenetics 53:59-63(2001).
DR	EMBL; AF329669; AAK11256.1; -.
DR	HSSP; P25947; 1CDP.
DR	MGD; MG1:193467; Tnfrsf12.
DR	InterPro; IPR000488; Death.
DR	InterPro; IPR000561; EGF-like.
DR	InterPro; IPR001368; TNFR_c6.
DR	Pfam; PF00531; death_1.
DR	Pfam; PF00030; TNFR_c6; 3.
DR	SMART; SM00005; DEATH; 1.
DR	SMART; SM00208; TNFR_3.
DR	PROSITE; PSS0017; DEATH DOMAIN; 1.

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DR PROSITE; PS01186; EGF 2; UNKNOWN 1.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN 1
DR PROSITE; PS00050; TNFR_NGFR_2; 1.
SQ SEQUENCE 413 AA; 44453 MW; 69F21B8ED0DABAF CRC64,

Query Match 21.5%; Score 202; DB 11; Length 413;
Best Local Similarity 31.4%; Pred No 2 3e-14;
Matches 48; Conservative 19; Mismatches 58; Indels 28; Gaps 7.

QY 18 CCTKTKTKTYLYNCPDQDTCPCFSGSFTASENHLR-HGLSCSKCPKEMGQVEISS 76
Db 54 CUREGPGHYKAPCAEDPCNSTGLPQSDTLTPNHFYDTPCQVCTDEALQVTLEN 113
QY 77 CTVDRTDTCGCKNQRYHWSENI-PQCFNCSLCLNG-TVHLSC-----QKQNTVCT 127
Db 114 CSAKSDTHGQSG-----W-----CVD-STVPCGKSSPFCVPGGATTPVHEATPRP 162
QY 128 CHAGFFLENECVSC-----SNCKKSLECTKLC 155
Db 163 CLPQGYIRGNDCTCPTGFSVCPKA--CTAVC 193

RESULT 5
Q9PVD4 PRELIMINARY; PRT; 387 AA.
AC Q9PVD4;
DT 01 MAY-2000 (Tremblrel. 13, Created)
DT 01 MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01 JUN 2001 (Tremblrel. 17, Last annotation update)
DR P75 like transmembrane protein fullback.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi,
OC Amphibia; Batrachia, Anura, Mesobatrachia, Pipidea, Pipidae,
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Hick F., Sun R. I., Collins-Paie L., Javallie E., Sive H. I.;
RT "Identification and characterization of fullback, a novel posteriorly-
RT expressed Xenopus gene".
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF131850; AAC54072.1.
DR HSSP; P07174; INGR.
DR InterPro; IPR001081; Copper-fist
DR InterPro; IPR000488; Death.
DR InterPro; IPR001368; TNFR_C6.
DR Pfam; PF00531; death; 1.
DR Pfam; PF00020; TNFR_C6; 4.
DR SMART; SM00412; C1_FIST; 1.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS00017; DEATH DOMAIN; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN 3.
DR PROSITE; PS00050; TNFR_NGFR_2; 4.
KW Transmembrane.
SQ SEQUENCE 387 AA; 42066 MW; 1A386A239C7C8A82 CRC64;

Query Match 20.5%; Score 193; DB 13; Length 387;
Best Local Similarity 31.9%; Pred No 2 2e-13;
Matches 53; Conservative 24; Mismatches 71; Indels 18; Gaps 10.

QY 1 DSVCPQRYVHPNNSICTYCHQTYLYNCPDQDTCPCFSGSFTASENHLPHC 59
Db 22 EAVVSEGLY---TNSGKQCSLCPAGPQVVPD---GSDSTCFPCISNTESDVPSAPAK 76
QY 60 LSCSKCPKEMGQVEISSCTVDRTDTCGCKNQRYHWSENI-PQCFNCSLCLNG-TVHLSC 118
Db 77 CUREGPGHYKAPCAEDPCNSTGLPQSDTLTPNHFYDTPCQVCTDEALQVTLEN 131
QY 110 CFFQNTVC-TCHAGFLP-----ENECVSC-SNCKKSLECTKLC 158
Db 132 THNKNTVQLSSGYSYSEVSWKSSPCLPCTPCQVETEVQIGDCVQ 177

Query Match 20.3%; Score 191; DB 11; Length 433;
Best Local Similarity 32.7%; Pred. No. 4e-13;
Matches 52; Conservative 18; Mismatches 79; Indels 10; Gaps 7.

QY 4 CPQGYVHPNNSICTYCHQTYLYNCPDQDTCPCFSGSFTASENHLPHC 62
Db 20 CQISQSYVYVYACMCAPCPDQDTCPCFSGSFTASENHLPHC 74
QY 63 SKCFKEMGQVEISSCTVDRTDTCGCKNQRYHWSENI-PQCFNCSLCLNG-TVHLSC 119
Db 79 SSCSDG--QVETHNCTFKQNFVTAAGSGV-ALEKSGNFP-JWELKGRGR-HVAFAP 136
QY 120 EYQNTVCT-CHAGFFLENECVSCSNCFYSLEETFLCLP 157
Db 137 SNGNVICSACAPSTF--SDTTSTSDVCRPHRIGSILAIP 173

RESULT 7
Q9PUS0 PRELIMINARY; PRT; 302 AA.
AC Q9PUS0;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01 JUN-2002 (Tremblrel. 21, Last annotation update)
DE Decoy TNF receptor.
OS Salvelinus fontinalis (Brook trout) (Brook char).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Tricacanthopterygii; Salmoniformes; Salmonidae; Salvelinus.
OX NCBI_TaxID=8038;
RN [1]
RP SEQUENCE FROM N.A.
RA Bobe J., Goetz F.W.;
RT "A tumor necrosis factor decoy receptor homologue is up regulated in
RT the brook trout (Salvelinus fontinalis) ovary at the completion of
RT ovulation.".
RL Biol. Reprod. 42:420-426(2000).
DR EMBL; AF156738; AAD56428.1; -.
DR HSSP; O14763; ID4V.
DR InterPro; IPR000561; EGF like.
DR InterPro; IPR001368; TNFR_C6.

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RA Pickup D.J., Bastia D., Stone H O., Joklik W K ;  
 RT "Sequence of terminal regions of cowpox virus DNA: arrangement of  
 PT repeated and unique sequence elements."  
 RL Proc Natl Acad Sci U S A 73:7112-7116(1982).  
 RN [13]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BRIGHTON RED;  
 RX MEDLINE=90177240; PubMed=2109453;  
 RA Parsons B.L., Pickup D.J.;  
 RT "Transcription of orthopoxvirus telomeres at late times during  
 RT infection."  
 RL Virology 175:69-80(1990).  
 RN [14]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BRIGHTON RED;  
 RX MEDLINE=91196263; PubMed=2014645;  
 RA Hu F.Q., Pickup D.J.;  
 RT "Transcription of the terminal loop region of vaccinia virus DNA is  
 RT initiated from the telomere sequences directing DNA resolution."  
 RL Virology 181:716-720(1991).  
 RN [15]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BRIGHTON RED;  
 RX MEDLINE=94378510; PubMed=8091665;  
 RA Hu F.Q., Smith C.A., Pickup D.J.;  
 RT "Cowpox virus contains two copies of an early gene encoding a soluble  
 RT secreted form of the type II TNF receptor".  
 RL Virology 204:343-356(1994).  
 RN [16]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BRIGHTON RED;  
 RA Pickup D.J.;  
 RT Submitted (AUG-1993) to the EMBL/GenBank/DBJ databases.  
 RN [17]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BRIGHTON RED;  
 RA Dietrich F.S., Ray C.A., Sharma A.D., Allen A., Pickup D.J.;  
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; U87234; AAB94344.1;  
 DR EMBL; AF482758; AAM13659.1;  
 DR HSP; 014763; IDOG.  
 DR InterPro: IPR001368; TNFR\_c6.  
 DR Pfam: PF00020; TNFR\_c6; 2.  
 DR SMART: SMO0208; TNFR; 2.  
 DR PROSITE: PS00652; TNFR\_NGFR\_1; 2.  
 DR PROSITE: PS50050; TNFR\_NGFR\_2; 2.  
 KW Receptor.  
 SQ SEQUENCE 320 AA; 35234 MW; AA0DF0CR47F7AB6 CRC64;  
 Query Match 18.8%; Score 176.5; DB 12; Length 320;  
 Best Local Similarity 27.8%; Pred. No. 1.2e-11;  
 Matches 42; Conservative 22; Mismatches 62; Indels 25; Gaps 6,  
 QY 14 NNSIGCTKCHKTYLVNDRPGPDTTCPECSSTASENHLEHCLSCSKCKPKWQV 72  
 Db SNNLCKQCDPGMYMTHSC-NTTSKDKCDPDGTFSTIPNHPTCJSCGKCS--SNHV 94  
 QY 73 ELSCTVDPTVCGCPFNQPHYWSENLPQCFNGLGNGTWHLSQCFQNTVCTCHAGF 132  
 Db ETKSCSNTQDRVCVAGSYVCFRGSN-----GFLCPVPT-----KCDGGY 136  
 QY 133 FL---PENEVCSCNCKYSLETKYLCLEQIE 160  
 Db GVGYSYSGKGVTCRKPQGNINDVCDLSPNSID 167  
 RESULT 11  
 Q62327 PRELIMINARY; PRT; 459 AA.  
 AC Q62327  
 DT 01 NOV 1996 (TRENBLrel. 01, Created)  
 DT 01 NOV 1996 (TRENBLrel. 01, Last sequence update)  
 DT 01 JUN 2002 (TRENBLrel. 21, Last annotation update)

DE Murine tumour necrosis factor receptor 2 protein (Fragment).  
 GN TNFRSF1B.  
 OS Mus musculus (Mouse).  
 OC Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OC NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=NOD;  
 RA Powell E.B., Wicker L.S., Peterson L.B., Todd J.A.;  
 RT "Amino acid variation in the tumor necrosis factor receptor 2 is  
 RT linked to autoimmune diabetes in NOD mice."  
 RL Genomics 0:0-0(0).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=NOD;  
 RX MEDLINE=95178848; PubMed=7873884;  
 RA Powell E.B., Wicker L.S., Peterson L.B., Todd J.A.;  
 RT "Allelic variation of the type 2 tumor necrosis factor receptor  
 RT gene."  
 RL Mamm. Genome 5:726-727(1994).  
 DR EMBL; X76401; CAA53981.1;  
 DR HSP; P19438; INCF.  
 DR MGD, MGI:1324883; Infrsfib.  
 DR InterPro: IPR001368; TNFR\_c6.  
 DR Pfam: PF00020; TNFR\_c6; 4.  
 DR SMART: SMO0208; TNFR; 4.  
 DR PROSITE: PS00652; TNFR\_NGFR\_1; 2.  
 DR PROSITE: PS50050; TNFR\_NGFR\_2; 3.  
 KW Receptor.  
 FT NON TER 1 1  
 FT VARIANT 87 87 S -> T.  
 FT VARIANT 93 93 T -> I.  
 FT VARIANT 268 268 F -> I.  
 FT VARIANT 345 345 S -> F.  
 FT VARIANT 421 421 Y -> C.  
 SQ SEQUENCE 459 AA; 48686 MW; 6C51D2CF1C4626DF CRC64;  
 Query Match 18.7%; Score 176; DB 11; Length 459;  
 Best Local Similarity 31.1%; Pred. No. 2e-11;  
 Matches 50; Conservative 20; Mismatches 77; Indels 14; Gaps 8;  
 QY 4 CPQKYIHPQNNSTCCTKCHKTYLVNDRPGPDTTCPECSSTASENHLEHCLSC 62  
 Db CQISGEVYDPRKQMCAPCPFPQVVFHPQ NPTSDTWALCEA:MYTCVMNQPKETLAE 84  
 QY 63 SKCRKEMGQVELSCTVHPDTVCGCPFNQY----PQVWSLENLPQCFNGLG 117  
 Db SSCSTD--QVETRACTKQNVCAEAGPYCALKTH SSCCFQCPPLSKGQHGPGVANS 139  
 QY 118 COEKONTVC-ACHAGFFLFENEVCVSCNCKYSLETKYLCLEP 167  
 Db RAPNGNVLCACAPGT--SDTTSSTDVCPHRCISILAI 178  
 RESULT 12  
 Q9DGH8  
 ID Q9DGH8 PPELIMINARY; PRT; 312 AA.  
 AC Q9DGH8  
 DT 01-MAR-2001 (TRENBLrel. 16, Created)  
 DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)  
 DT 01-DEC-2001 (TRENBLrel. 16, Last annotation update)  
 DE Fas antigen (Fragment).  
 GN FAS.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Bridgman J.T., Johnson A.L.;  
 RT "Fas Expression and Regulation in Ben Granulosa Cells.";







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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: January 6, 2003, 04:09:12 ; Search time 2808 Seconds  
(without alignments)  
1668.644 Million cell updates/sec

Title: US-09-882 735 2  
Perfect score: 941  
Sequence: 1 DSVCPQKYYHPQNNISICT CSNCKKSLCTKLCPLQIEN 161

Scoring table:  
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Xgapop 10.0, Xgapext 0.5  
Ygapop 10.0, Ygapext 0.5  
Zgapop 6.0, Zgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

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-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenEmbl :  
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2: gb\_htg :  
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4: gb\_ov :  
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8: gb\_pl :  
9: gb\_pr :  
10: gb\_ro :  
11: gb\_sts :  
12: gb\_sy :  
13: gb\_un :  
14: gb\_vl :  
15: em\_ba :  
16: em\_fun :  
17: em\_hum :  
18: em\_in :  
19: em\_mu :  
20: em\_ov :  
21: em\_ov :  
22: em\_ov :  
23: em\_pat :  
24: em\_ph :  
25: em\_pl :  
26: em\_ro :  
27: em\_sts :  
28: em\_un :

29: em\_vl :  
30: em\_htg\_hum :  
31: em\_htg\_inv :  
32: em\_htg\_other :  
33: em\_htg\_mus :  
34: em\_htg\_pln :  
35: em\_htg\_rod :  
36: em\_htg\_mam :  
37: em\_htg\_vrt :  
38: em\_sy :  
39: em\_htgo\_hum :  
40: em\_htgo\_mus :  
41: em\_htgo\_other :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	941	100.0	483	6	A29099 Sequence
2	941	100.0	483	6	AR174442 Sequence
3	941	100.0	1301	6	AR1131310 Sequence
4	941	100.0	1301	6	AR1134762 Sequence
5	941	100.0	1331	6	A29103 Sequence
6	941	100.0	1368	6	A29098 Sequence
7	941	100.0	2050	9	HUMTNFRP
8	941	100.0	2062	6	A21522
9	941	100.0	2062	6	I43805 Sequence
10	941	100.0	2087	9	HUMTNFR
11	941	100.0	2109	9	AF056611
12	941	100.0	2111	6	A26412
13	941	100.0	2111	6	AX409713 Sequence
14	941	100.0	2111	9	HUMTNFRB
15	941	100.0	2112	9	HUMTNFRB
16	941	100.0	2161	6	AP006330
17	941	100.0	2161	9	HSTNFR1A
18	941	100.0	2175	6	A43873
19	941	100.0	2175	6	A78738 Sequence
20	941	100.0	2175	6	AR041076
21	941	100.0	2175	6	I64751
22	941	100.0	2176	6	A19207
23	941	100.0	2194	9	BC010140
24	941	100.0	6899	6	I26928 Sequence
25	941	100.0	6896	6	AP011375
26	941	100.0	6896	6	BD009743
27	930	98.8	510	6	A21525
28	930	98.8	510	6	A29257
29	928	98.6	1147	6	AR1131309
30	928	98.6	1147	6	AR1134761
31	924	98.2	600	6	I43808
32	914	97.1	2061	6	A29255
33	842.5	89.5	1049	6	AR1131307
34	842.5	89.5	1049	6	AR1134759
35	837	88.9	1202	6	AR1131308
36	837	88.9	1202	6	AR1134760
37	780	82.9	2171	4	AB051103
38	756	80.3	572	4	AF013955
39	746	79.3	501	6	I43786
40	746	79.3	501	6	A20713
41	746	79.3	504	6	I43813
42	746	79.3	1977	6	AX404869
43	736	78.2	597	6	AX455662
44	731	77.7	372	6	A20253
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ALIGNMENTS

RESULT 1



TITLE Hybrid heterodimeric protein hormone  
JOURNAL Patent: US 619372-A 7 27-FEB-2001;  
FEATURES Location/Qualifiers

source 1..1301  
BASE COUNT 269 a 413 c 351 g 268 t  
ORIGIN

Alignment Scores:  
Pred. No.: 1,45e-79 Length: 1301  
Score: 941.00 Matches: 161  
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Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0

US 09,882,735-2 (1-161) x AR131310 (1-1301)

QY 1 AspSerValCysProGlnGlyTyrIleHisProGlnAsnAsnSerIleCysCysThr 20  
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QY 21 LysCysHisLysGlyThrTyrLeuTyrAsnAspCysProGlyProGlyGlnAspThrAsp 40  
Db 405 AASTGCTCAAAAGAAACCTAATTGTACAAATGACTGTCCAGGCCCGGGCGAGATACCGGAC 464  
QY 41 CysArgGluCysGluSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu 60  
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QY 61 SerCysSerLysCysArgLysGluMetGlyGlnValGluIleSerSerCysThrValAsp 80  
Db 525 AGCTGCTTCAAAATGCTGAAAGAAAATATATATAGGTGGAGATCTCTCTTGACACAGTGGAC 584  
QY 81 ArgAspThrValCysGlyCysArgLysAsnGlnTyrArgHisTyrTrpSerGluAsnLeu 100  
Db 585 CGTAAATGCTGTAT 644  
QY 101 PheGlnCysPheAsnCysSerLeuAsnGlyThrValHisLeuSerCysGlnGlu 120  
Db 645 TTCCAGTGTCTCAATTCAGGCTCTGCTCAATGAGACGCTGACCTCTCTCTGCGCAGGAG 704  
QY 121 LysGlnAsnThrValCysThrCysHisAlaGlyPhePheLeuArgGluAsnGluCysVal 140  
Db 705 AAACAGAAACGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 764  
QY 141 SerCysSerAsnCysLysLysSerLeuGluCysThrLysLeuCysLeuProGlnIleGlu 160  
Db 765 TCCTGTAGTAATCTTAAGAAAAGCTGAGTGCAGCAAGTTGTGCTTACCCCAAGTTGAG 824

RESULT 4  
AR134762 AR134762 1301 bp DNA linear PAT 16-MAY-2001  
LOCUS  
DEFINITION Sequence 7 from patent US 6194177.  
ACCESSION AR134762  
VERSION AR134762.1 GI:14123667

KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 1301)  
AUTHORS Campbell, R. K., Jameson, R. A., and Chappel, S. C.  
TITLE DNA encoding a hybrid heterodimeric protein  
JOURNAL Patent: US 6194177-A 7 27-FEB-2001,  
FEATURES Location/Qualifiers  
source 1..1301  
/organism="unknown"

BASE COUNT 269 a 413 c 351 g 268 t  
ORIGIN

## Alignment Scores:

Pred. No.: 1,45e-79 Length: 1301  
Score: 941.00 Matches: 161  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0

US 09,882,735-2 (1-161) x AP134762 (1-1301)

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QY 41 CysArgGluCysGluSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu 60  
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QY 61 SerCysSerLysCysArgLysGluMetGlyGlnValGluIleSerSerCysThrValAsp 80  
Db 525 AGCTGCTTCAAAATGCTGAAAGAAAATATATATAGGTGGAGATCTCTCTTGACACAGTGGAC 584  
QY 81 ArgAspThrValCysGlyCysArgLysAsnGlnTyrArgHisTyrTrpSerGluAsnLeu 100  
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Db 705 AAACAGAAACGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 764  
QY 141 SerCysSerAsnCysLysLysSerLeuGluCysThrLysLeuCysLeuProGlnIleGlu 160  
Db 765 TCCTGTAGTAATCTTAAGAAAAGCTGAGTGCAGCAAGTTGTGCTTACCCCAAGTTGAG 824

RESULT 5  
A29103 A29103 1331 bp DNA linear PAT 03-JUL-1996  
LOCUS  
DEFINITION H.sapiens mRNA for TNF-binding polypeptide from patient EP049448  
ACCESSION A29103  
VERSION A29103.1 GI:1247517

KEYWORDS

SOURCE Homo sapiens.

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE 1 (bases 1 to 1331)

AUTHORS Hauptmann, R., Himmler, A., Maurer-Pegib, I., and Striatowa, C.

TITLE TNF-receptor, TNF-binding protein and DNA coding therefor

JOURNAL Patent: EP 039438-A 53 24-OCT-1990;

BOEHRINGER INGELHEIM INTERNATIONAL G.M.B.H.

FEATURES

Location/Qualifiers

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US-09-882-735-2 (1-161) x A29098 (1-1368)

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 DB 513 AGTGTCTTCAAAATTCGAAAGAAATTCGATCAGTGTGAGATCTCTTCTTGCAAGTGAGAC 572  
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 QY 161 Asn 161  
 DB 813 AAT 815

RESULT 6  
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 LOCUS A29098 1368 bp DNA linear PAT 03-JUL-1995  
 DEFINITION Synthetic DNA for TNF-receptor from patent EP0393438.  
 ACCESSION A29098  
 VERSION 1  
 KEYWORDS

ORGANISM  
 SOURCE  
 ORGANISM  
 REFERENCE  
 1 (bases 1 to 1368)  
 AUTHORS Hauptmann, P., Himmeler, A., Maurer-Fogy, I. and Stratowa, C.  
 TITLE TNF-receptor, TNF-binding protein and DNA coding therefor  
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 87 (19), 7380-7384 (1990)  
 COMMENT

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US-09-882-735-2 (1-161) x A29098 (1-1368)

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 QY 21 LysCysHisLysGlyThrTyrLeuTyrAsnAspCysProGlyProGlyGlnAspThrAsp 40  
 DB 181 AAGTGTCCAAAGAAAGAACTACTTGTACATATACATGTCCAAAGCCGAGGATACGAGAC 240  
 QY 41 CysArgGluCysGlnSerGlySerPheThrAlaSerGlnAsnHisLysArgHisCysLeu 60  
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 DB 301 AGTGTCTTCAAAATTCGAAAGAAATTCGATCAGTGTGAGATCTCTTCTTGCAAGTGAGAC 360  
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 DB 361 CGGAAACCGGT 420  
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 QY 121 LysGlnAsnThrValCysThrCysHisAlaGlyPhePheLeuArgGlnAsnGluCysVal 140  
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 QY 141 SerCysSerAsnCysLysLysSerLeuGluCysThrLysLeuCysLeuProGlnIleGlu 160  
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 DB 601 AAT 603

RESULT 7  
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 DEFINITION Human tumor necrosis factor receptor (TNF) mRNA, complete cds.  
 ACCESSION M60275 M37764  
 VERSION 1  
 KEYWORDS  
 TNF receptor; transmembrane receptor; tumor necrosis factor receptor.

SOURCE  
 ORGANISM  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 REFERENCE  
 1 (bases 1 to 2050)  
 AUTHORS Gray, P.W., Barrett, K., Chantry, D., Turner, M. and Feldmann, M.  
 TITLE Cloning of human tumor necrosis factor (TNF) receptor cDNA and expression of recombinant soluble TNF-binding protein  
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 87 (19), 7380-7384 (1990)  
 MEDLINE  
 PUBMED  
 2170974

COMMENT  
 Draft entry and computer-readable sequence for [Proc. Natl. Acad. Sci. U.S.A. (1990) in press] kindly submitted by P.W.Gray, 13-AUG-1990.

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sign pent ide

274

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237, 1474
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mat rept ide

275. 1513

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/product="TNF receptor"

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Best local Similarity:	100.00%
Query Match:	100.00%
BB:	9
Gaps:	0
Indels:	0
Mismatches:	0
Conservative:	0
Matches:	161
Length:	2050

US 09 882-735-2 (1-161) x HUMTNFRP (1-2050)

Qy 1 AspSerValCysProGlnGlyLysTyrIleHisProGlnAsnAsnSerIleCysCysThr 20

21 LysCysHisLysGlyThrTyrLeuTyrAsnAspCysProGlyProGlyGlnAspThrAsp 40

335 AAGTGCTACAAATGAACTTACTTGTACCAATGACTGTCCAGGCCGGGGCAGGATACGGAC 394

41 CysArgGluCysGluSerGlySerPheThrAlaSerGluAspHisLeuArgHisCysLeu 60

DB 195 TGGAGGAGTGTGATAGAGGAGGTTTAAATGTTCAIAAAACCACTTATAGAGACTGCT 454

**LECTURE 2**

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Qy 81 ArgAspThrValCysGlyCysArgLysAsnGlnTyrArgHisTyrTrpSerGluAsnLeu 100

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639

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Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
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BASE COUNT
ORIGIN

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Alignment Scores:
Pred. No.:      2.4e-79
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Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match:    100.00%
DB:             6
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Gaps:
US-09-882-735 2 (1 161) X A21522 (1 2062)

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[illegible]

[illegible]

REFERENCE	TITLE	JOURNAL	FEATURES
AUTH:RS		MEDLINE	source
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		COMMENT	
1 (bases 1 to 2087)	Mammalia: Eutheria; Primates; Catarrhini; Hominoidea; Homo.	99235285	Cell 61 (2), 361-370 (1990)
Goedel, D.V.	necrosis factor		
Gatanaga, T., Granger, G.A., Lentz, R., Raab, H., Kohr, W.J. and			
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by T.Schall, 26-MAR-1990.			
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FFGLCLSLILFGLMYRQWMSKLSIVCGSTPEKGELEGTTRKPLAPNSPS			
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Lb	442	TGCACAGGAGTGTACAGCCCTCTCTTCAACCCCTTCACAAACCAACCTGACACAGCGCC	481
QY	61	SerCysSerIstCysArgIstGlnMetArgIstGlnValGulIleSerSerCysThrValAsp	80
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Lb	662	AAACCAACCAACCTCTGACCTGACATACAGTTCCTTCTTACCAACCAACCAACCTGTC	721
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Best Local Similarity: 100.00% Mismatches: 0  
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US-09-882-735-2 (1161) x AX409713 (1-2111)

QY 1 AspSerValCysProGlnGlyLeuTyrLeuHisProGlnAsnAsnSerIleCysCysThr 20  
DB 307 GATAGTGTGTCTCCCAAGGAAAAATATATCCACCCCTTAATATGATTTGCTGTAC 366  
QY 21 LysCysHisLysGlyTyrThrTyrLeuTyrAsnAspCysProGlyProGlyGlnAspThrAsp 40  
DB 367 AAGTCCCAAGAACCACTACTGTATACAAATGATGTCAGGAGGAGGAGGAGGAGGAG 426  
QY 41 CysArgGluCysGlySerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu 60  
DB 427 TGCAGGAGGTGTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 486  
QY 61 SerCysSerLysCysArgLysGluMetGlyGlnValGlnIleSerSerCysThrValAsp 80  
DB 487 AGTGTCTCAATATCCCAAGGAAATGGTCAAGTGGAGATCTCTTCTTGACAGTGGAC 546  
QY 81 ArgAspThrValCysGlyCysArgLysAsnGlnTyrArgHisTyrTrpSerGluAsnLeu 100  
DB 547 CGGACACCGGT 606  
QY 101 PheGlnCysPheAsnGlySerLeuAsnGlyTyrValHisLeuSerCysGlnGlu 120  
DB 607 TTCCAGTCTCTCAATATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 666  
QY 121 LysGlnAsnThrValCysThrCysHisAlaGlyPhePheLeuArgGluAsnGluCysVal 140  
DB 667 AAACGAGAACCGGT 726  
QY 141 SerCysSerAsnGlyLysSerLeuGluCysThrHisLeuCysLeuProGlnIleGlu 160  
DB 727 TCTGTACTACTGTATAGAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 786  
QY 161 Asn 161  
DB 787 AAT 789

RESULT 14  
AX409713 2111 bp DNA linear PAT 14-JUN-2002  
LOCUS AX409713  
DEFINITION Homo sapiens tumor necrosis factor receptor mRNA, complete cds.  
ACCESSION AX409713  
VERSION AX409713.1 GI:21442418  
KEYWORDS  
SOURCE human  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
1 Alvarez, C., Horne, D., Perez-da-Silva, S. and Vockley, J. G.  
TITLE Gene expression profiles in liver cancer  
JOURNAL Parent: WJG 2003; 13: 11-15  
GENE LOGIC INC (US)  
FEATURES  
source location/Qualifiers  
1..2111  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/note="EMBL/GenBank Accession No. M58286"

BASE COUNT 445 A 629 C 587 G 450 T  
ORIGIN  
Alignment Scores:  
Fred. No.: 2.46e 79 Length: 2111  
Score: 941.00 Matches: 161  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0

US-09-882-735-2 (1161) x AX409713 (1-2111)

QY 1 AspSerValCysProGlnGlyLeuTyrLeuHisProGlnAsnAsnSerIleCysCysThr 20  
DB 307 GATAGTGTGTCTCCCAAGGAAAAATATATCCACCCCTTAATATGATTTGCTGTAC 366  
QY 21 LysCysHisLysGlyTyrThrTyrLeuTyrAsnAspCysProGlyProGlyGlnAspThrAsp 40  
DB 367 AAGTCCCAAGAACCACTACTGTATACAAATGATGTCAGGAGGAGGAGGAGGAGGAG 426  
QY 41 CysArgGluCysGlySerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu 60  
DB 427 TGCAGGAGGTGTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 486  
QY 61 SerCysSerLysCysArgLysGluMetGlyGlnValGlnIleSerSerCysThrValAsp 80  
DB 487 AGTGTCTCAATATCCCAAGGAAATGGTCAAGTGGAGATCTCTTCTTGACAGTGGAC 546  
QY 81 ArgAspThrValCysGlyCysArgLysAsnGlnTyrArgHisTyrTrpSerGluAsnLeu 100  
DB 547 CGGACACCGGT 606  
QY 101 PheGlnCysPheAsnGlySerLeuAsnGlyTyrValHisLeuSerCysGlnGlu 120  
DB 607 TTCCAGTCTCTCAATATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 666  
QY 121 LysGlnAsnThrValCysThrCysHisAlaGlyPhePheLeuArgGluAsnGluCysVal 140  
DB 667 AAACGAGAACCGGT 726  
QY 141 SerCysSerAsnGlyLysSerLeuGluCysThrHisLeuCysLeuProGlnIleGlu 160  
DB 727 TCTGTACTACTGTATAGAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 786  
QY 161 Asn 161  
DB 787 AAT 789

RESULT 14  
HUMTNFRB 2111 bp mRNA linear PRI 03-AUG-1993  
LOCUS HUMTNFRB  
DEFINITION Homo sapiens tumor necrosis factor receptor mRNA, complete cds.  
ACCESSION M58286 M33480  
VERSION M58286.1 GI:339753  
KEYWORDS  
SOURCE human cell line HU60, cDNA to mRNA.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
1 Leutscher, H., Par, Y. C., Loh, H. W., Gell, C. F., Brockhaus, M.,  
Taduchi, H. and Lesslauer, W.  
TITLE Molecular cloning and expression of the human 55 kd tumor necrosis  
JOURNAL factor receptor  
MEDLINE Cell 61 (2), 351-359 (1990)  
PUBMED 2158862  
FEATURES  
source location/Qualifiers  
1..2111  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/cell\_line="HU60"  
1..2111  
/gene="TNF receptor"  
187..1554  
/gene="TNF receptor"  
/note="55 kDa"  
/codon\_start=1  
/product="tumor necrosis factor receptor"  
/protein\_id="AA36753.1"  
/db\_xref="GI:339754"  
/translation="MGLSTVPDLPLPLVLELLVGIYPSVITGLVPHLGDPEPPDSVC



Mon Jan 6 08:48:27 2003

us-09-882-735-2.rge

Page 10

[illegible]

Search completed: February 6, 2007, 06:07:28  
Job time : 2835 secs

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.





Query Match: 100.00% Indels: 0  
 PIR: 19 Gaps: 0

US-09-882-735-2 (1-161) x AAV19801 (1-483)

QY 1 AspSerValCysProGlnGlyTyrIleHisProGlnAsnSerIleCysThr 20  
 DB 1 CATAGTGTCTCTCCCAAGAAAATATATCCACCTCAAAATAATTCGATTGCTGACC 60

QY 21 LysCysHisLysGlyThrTyrLeuTyrAsnAspCysProGlyProGlnGlnAspThrAsp 40  
 DB 61 AACTGTCACAAAGAAATCTACTTGTACAAATGACTGTCCAGGCTCCGGGACAGGATACGAC 120

QY 41 CysArgGluCysGluSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu 60  
 DB 121 TCAAGGATTTGAG 180

QY 61 SerCysSerLysCysArgGluMetGlyGlnValGluIleSerSerCysThrValAsp 80  
 DB 181 AGTGTCTCAAAATGCGCAAGGAAATGATGATGATGATGATGATGATGATGATGATGAT 240

QY 81 ArgAspThrValCysGlyCysArgLysAsnGlnTyrArgHisTyrTrpSerGluAsnLeu 100  
 DB 241 GAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 300

QY 101 PheGlnCysPheAsnSerLysCysLeuAsnGlyThrValHisLeuSerCysGlnGlu 120  
 DB 301 TTCCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCAT 360

QY 121 LysGlnAsnThrValCysThrCysHisAlaGlyPhePheLeuArgGluAsnGluCysVal 140  
 DB 361 AAAAATAACAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420

QY 141 SerCysSerAsnCysLysLysSerLeuGluCysThrLysLeuCysLeuProGlnIleGlu 160  
 DB 421 TCCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480

QY 161 Asn 161  
 DB 481 AAT 483

RESULT 3  
 ID AAV81732 standard; cDNA; 483 BP.  
 AC AAV81732;  
 DT 04 MAR 1999 (first entry)  
 DE Tumour necrosis inhibitor 30 kDa encoding cDNA.  
 XX  
 FW Tumour necrosis factor receptor 1; TNFR 1; inhibitor; osteoprotegerin;  
 KW OPG; chimeric; fusion; dimerisation domain; autoimmune disease;  
 KW inflammation; apoptosis; ss.  
 XX  
 CS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 1..483  
 FT /\*tag= a  
 FT /note= "no stop codon given"  
 XX  
 FN WC9949305-A1  
 XX  
 PD 05 NOV-1998.  
 XX  
 PF 29-APR-1998; 98WO-US08631.  
 XX  
 PR 01 MAY-1997; 97US-085018A  
 XX  
 PA (AMGEN) AMGEN INC.  
 XX  
 PI Boyle WJ, Wooden S;

XX WPI: 1999-034661/03.  
 DR P-PSDB; AAM89233.  
 XX New chimeric osteoprotegerin polypeptides - contain the  
 PT osteoprotegerin dimerisation domain and a heterologous sequence,  
 PT useful to treat TNF and TNFR-mediated disorders  
 XX Disclosure; Fig 2; 92pp; English.

XX The present invention describes a chimeric polypeptide (AI), comprising  
 CC an osteoprotegerin (OPG) dimerisation domain fused to a heterologous  
 CC amino acid sequence. Also described are: (1) a multimer polypeptide  
 CC comprising covalently associated AI monomers; (2) an isolated nucleic  
 CC acid encoding AI; (3) an expression vector comprising the nucleic acid  
 CC sequence; and (4) a host cell transformed or transfected with the  
 CC expression vector so that the nucleic acid is expressible. The products  
 CC from the present invention are useful to treat a variety of disorders  
 CC including those related to receptor binding. Compositions comprising  
 CC tumour necrosis factor (TNF)/OPG and TNF receptor (TNFR)/OPG dimers  
 CC are used to treat TNF and TNFR-mediated disorders such as inflammation,  
 CC autoimmune diseases and disorders related to excessive apoptosis. The  
 CC chimeras are also useful for detecting molecules which interact with  
 CC fused heterologous sequences to identify potential new receptors and  
 CC ligands. The present sequence encodes the TNF inhibitor 30 kDa protein.

XX Sequence 483 BP; 130 A; 124 C; 123 G; 106 T; 0 other;

Alignment Scores:  
 Pred. No.: 9,46e-79 Length: 483  
 Score: 941.00 Matches: 161  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 20 Gaps: 0

US-09-882-735-2 (1-161) x AAV81732 (1-483)

QY 1 AspSerValCysProGlnGlyLysTyrIleHisProGlnAsnSerIleCysThr 20  
 DB 1 CATAGTGTCTCTCCCAAGAAAATATATCCACCTCAAAATAATTCGATTGCTGACC 60

QY 21 LysCysHisLysGlyThrTyrLeuTyrAsnAspCysProGlyProGlnGlnAspThrAsp 40  
 DB 61 AAGTCCACCAAGGAGACCTACTTGTATCAATGACTGTCCAGGCTCCGGGACAGGATACGAC 120

QY 41 CysArgGluCysGluSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu 60  
 DB 121 TGCAGGAGGTGTGAG 180

QY 61 SerCysSerLysCysArgLysGluMetGlyGlnValGluIleSerSerCysThrValAsp 80  
 DB 181 AGTGTCTCAAAATGCGCAAGGAAATGATGATGATGATGATGATGATGATGATGATGAT 240

QY 81 ArgAspThrValCysGlyCysArgLysAsnGlnTyrArgHisTyrTrpSerGluAsnLeu 100  
 DB 241 CGGACACCGGT 300

QY 101 PheGlnCysPheAsnSerLysCysLeuAsnGlyThrValHisLeuSerCysGlnIleGlu 120  
 DB 301 TTCCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCAT 360

QY 121 LysGlnAsnThrValCysThrCysHisAlaGlyPhePheLeuArgGluAsnGluCysVal 140  
 DB 361 AACAGAACACCGGT 420

QY 141 SerCysSerAsnCysLysLysSerLeuGluCysThrLysLeuCysLeuProGlnIleGlu 160  
 DB 421 TCCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480

QY 161 Asn 161  
 DB 481 AAT 483

```

RESULT 4
AAC83945
ID AAC83945 standard: DNA; 483 BP.
XX
XX AAC83945;
AC
XX 02-MAR-2001 (first entry)
XX
XX Human 30 kDa TNF inhibitor coding sequence #1.
DE
XX TNF inhibitor; antiinflammatory; Tumour Necrosis Factor; interleukin;
XX IL-1; inflammatory disease; degenerative disease; human; ss.
XX
XX Homo sapiens.
XX OS
XX US6143866-A.
XX PN
XX 0/-NOV-2000.
XX PD
XX 19-JAN-1995; 95US-0375242.
XX PF
XX 19-JUL-1990; 90US-0555274.
XX PR
XX 09-JUL-1993; 93US-0090366.
XX PR
XX 18-JUL-1989; 89US-0381080.
XX PR
XX 11-DEC-1989; 89US-0450329.
XX PR
XX 07-FEB-1990; 90US-0479661.
XX
XX (AMGEN) AMGEN INC.
XX
XX Squires C, King MW, Hale KX, Brewer MT, Thompson RC;
PI Vanderelice RW, Varnice J, Kohno T;
XX WPI; 2001-006443/01.
XX DR
XX P-PSDB; AAB37676.
XX
XX Novel 30 kDa tumor necrosis factor inhibitor analog comprising a
PT non-native cysteine residue cross-linked with polyethylene glycol,
PT useful for treating inflammatory and degenerative diseases mediated by
PT TNF.
XX
XX Example 6, Fig 20, 82pp; English.
XX
XX The present invention relates to Tumour Necrosis Factor (TNF) inhibitors
XX (see AAB37676 and AAB37685), which have TNF inhibitory activity. The
XX novel TNF inhibitors of the present invention are useful as therapeutic
XX agents for inhibiting the activity of TNF and interleukin (IL-1), and
XX for treating inflammatory and degenerative diseases mediated by TNF. The
XX present sequence is the coding sequence for the 30 kDa TNF inhibitor
XX The 30 kDa TNF inhibitor can inhibit TNF alpha.
XX
XX Sequence 463 BP, 130 A, 124 C, 123 G, 106 T; 0 other.
SQ

Alignment Scores:
Pred. No.: 9,46e-79 Length: 483
Score: 941.00 Matches: 161
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 22 Gaps: 0

US-09-882-735-2 (1-161) x AAC83945 (1-483)
CY 1 ApsseVYVYcysproglnglytyrtyrlehisproglinsnasenrilecyscysThr 20
DB 1 CATAGTGTGTGTCCTCCCAAGAAATATATTCACCTCAAAATATTCGATTGTGTAC 60
CY 21 LysCysHisIysGlyThrTyrLeuTyrAsnAspCysProglYproglYglnAspThrAsp 40
DB 61 AAGTGTCCCAAGAGAACTTACTTGTATATGACTGTCCAGGCCGCGGATACGAAAC 120
CY 41 CysATG31uYcys31uSerGlySerPheThrAlaSerGluAsnHisLeuATGHisCysLeu 60

```

```

DB 121 TGCAGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAAACCACTTCAGACATGCTTC 180
CY 61 SerCysSerIysCysArgIysGluMetGlyGlnValGlnIleSerSerCysThrValAsp 80
DB 181 AGCTGCTCCAAATGCGCAAGAAAGAAATGGGTCAAGTGAATCTCTTCTTGACAGTGGAC 240
CY 81 ArgAspThrValCysGlyCysArgIysAsnGlnTyrArgHisTyrTrpSerGluAsnLeu 100
DB 241 CGGACACCGCTGTGTGCTGTGAGGAAAGAACCACTACCGGATATATGAGTCAAAACCTT 300
CY 101 PheGlnCysPheAsnGlySerLeuGlyCysLeuAsnGlyThrValHisSerSerCysGlnGlu 120
DB 301 TTCAGTCTCTCAATTGCAAGCTTGTGCTCAATGGAGACGTGACCTTCTGCGCAGGAG 360
CY 121 LysGlnAsnThrValCysThrCysHisAlaGlyPhePheLeuArgGluAsnGluCysVal 140
DB 361 AAACAGAAACCGCTGTGACCTGCGCATGCGAGTTCCTTCTTAAAGAAAAACGATGTGTC 420
CY 141 SerCysSerAsnGlyIysIysSerLeuGluCysThrIlyLeuGluCysLeuProGlnIleGlu 160
DB 421 TCTGTAGTAACTGTAAAGAAAGCTGAGTGCACGAAGTGTGTGCTTACCCAGATTGAG 480
CY 161 Asn 161
DB 481 AAT 483

RESULT 5
AAT94022
1D AAT94022 standard, cDNA; 1301 BP.
XX
XX AAT94022;
AC
XX 19-MAR-1998 (first entry)
XX
XX cDNA for TBP(20-190)/hCG-beta fusion protein.
XX
XX Fusion protein; thrombopoietin; TPO; human chorionic gonadotrophin;
XX beta subunit; hCG-beta; ss.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 279..1289
XX FT /*tag= a
XX
XX W09730161-A1.
XX
XX 21-AUG-1997.
XX
XX 20-FEB-1997; 97MO-US02315.
XX
XX 20-FEB-1996, 96US-0011936.
XX
XX (ISTF ) ARS APPLIED RES SYSTEMS HOLDING NV.
XX
XX Campbell FK, Chapel SC, Jameson BA;
XX WPI; 1997-425036/39.
XX DR P-PSDB; AAM33360.
XX
XX Hybrid dimeric protein comprising two co-expressed units - each
XX based on receptor or ligand and a subunit of a heterodimeric
XX hormone, especially FSH, for inducing follicular maturation
XX
XX Example; Pages 39-40; 60pp; English.
XX
XX A novel fusion protein comprises 2 dimer forming co-expressed amino
XX acid sequences, each consisting of a homodimeric or heterodimeric
XX receptor chain or ligand, with ligand-receptor binding activity,
XX bound directly or via a peptide linker to a subunit of a
XX heterodimeric protein hormone capable of forming a heterodimer with
XX the hormone's other subunits. The fusion protein, e.g. the
XX thrombopoietin (TPO)/human chorionic gonadotrophin-beta subunit
XX

```

CC (hcg beta) fusion protein encoded by the present sequence,  
 CC significantly increases the biological activity of the hormone  
 CC component, reducing the requirement for hormone itself and the  
 CC number of injections needed.

XX  
 SQ Sequence 1301 BP; 269 A; 413 C; 351 G; 268 T; 0 other;

## Alignment Scores:

Pred. No.: 3,27e-78 Length: 1301  
 Score: 941.00 Matches: 161  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 18 Gaps: 0

US-09-882-735-2 (1-161) x AAT94022 (1-1301)

OY 1 AspSerValCysProGlnGlyLysTyrIleHisProGlnAsnAsnSerIleCysCysThr 20  
 DB 345 GATAGTGTGTGTCCTCCCAAGGAAATATATCCACCTCAAAATAATTCGATTGCTGTACC 404  
 OY 21 LysCysHisLysGlyThrTyrLeuTyrAsnAspCysProGlyProGlyGlnAspThrAsp 40  
 DB 405 AAGTTCCTAAAGAGAACTATTTATTAATGACTGTCTAGGCTCGGGGACGATACGGAC 464  
 OY 41 CysArgGluCysGluSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu 60  
 DB 465 TGTAGGATTTATGAGTGTCTTCTACCTGCTTCAAGAAACCTCAGACACTGCTC 524  
 OY 61 SerCysSerLysCysArgLysGluMetGlyGlnValGluIleSerSerCysThrValAsp 80  
 DB 525 AGTGTCTTAAATGCTTAAAGTAAATGCTTAAAGTAAATGCTTAAAGTAAATGCTTAA 584  
 OY 81 ArgAspThrValCysGlyCysArgLysAsnGlnTyrArgHisTyrTrpSerGluAsnLeu 100  
 DB 585 GAGACACCGT 644  
 OY 101 PheGlnCysPheAsnCysSerLeuCysLeuAsnGlyThrValHisLeuSerCysGlnGlu 120  
 DB 645 TTTCCATCTTCTCAATTCAGATTTCTGTCTTAAATGCTTAAAGTAAATGCTTAAAG 704  
 OY 121 LysGlnAsnThrValCysThrCysHisAlaGlyPhePheLeuArgGluAsnGluCysVal 140  
 DB 705 AAACAGACATTTTATGAGT 764  
 OY 141 SerCysSerAsnCysLysLysSerLeuGluCysThrLysLeuCysLeuProGlnIleGlu 160  
 DB 765 TCTGTATGTAATTTATTAAGAAATGCTTAAAGTAAATGCTTAAAGTAAATGCTTAA 824  
 OY 161 Asn 161  
 DB 425 AAT 827

## RESULT 6

AA006282

ID AA006282 standard; DNA; 1334 BP.

AC

AA006282;

XX 29-JAN-1991 (first entry)

DT

DE Plasmid Tumour Necrosis Factor-Binding Protein 15 cDNA insert.

XX Tumour necrosis factor binding protein; TNF-BP; TNF receptor;

KW pTNF BP15; ss.

XX

OS Homo sapiens.

XX

PH Key Location/Qualifiers

FT 213..1325

FT /\*tag= a

FT /\*product=TNF-BP

XX

PN EP393438-A.  
 XX 24-OCT-1990.  
 XX 06-APR-1990; 90EP-0106624.  
 XX 21-JUN-1989; 89DE-390282.  
 XX 21-APR-1989; 89DE-3913101.  
 XX (BOEH) BOEHRINGER INGELHEIMINT.  
 PI Hauptmann R, Himmler A, Maurer Fooy I, Stratowa C;  
 XX WPI; 1990-321987/43.  
 DR P-PSDB; AAR07449.  
 XX DNA encoding TNF binding protein and TNF receptor used in  
 PT tumour treatment and to understand mechanism to TNF action  
 PS Disclosure; Fig 1(1-3); 51pp; German.  
 XX pTNF-BP15 is one of 30 positives clones in a screened cDNA library  
 CC from induced TNF-induced fibrosarcoma cells. A TNF BP had been  
 CC isolated from the urine of patients with trauma and probed/primer  
 CC were constructed from the determined amino acid sequence.  
 CC To produce a vector expressing a soluble form of TNF binding  
 CC protein, this plasmid was cut with XmnI, amplified by PCR and the  
 CC amplified DNA cut with BamHI and EcoRI.  
 CC The resulting 0.75 kb DNA fragment was inserted into pTZ19 alpha 19  
 CC (BSP) cut with the same enzymes to recover pTNF-BP. This was cut  
 CC with BamHI and EcoRI, and the recovered fragment inserted into  
 CC pAD-CMV1 (AA006283) to give the required plasmid pADTNF-BP.  
 CC See also AA006282-Q06285.  
 SQ Sequence 1334 BP; 299 A; 409 C; 342 G; 284 T; 0 other;

## Alignment Scores:

Pred. No.: 3,38e-78 Length: 1334  
 Score: 941.00 Matches: 161  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 11 Gaps: 0

US-09-882-735-2 (1-161) x AA006282 (1-1334)

OY 1 AspSerValCysProGlnGlyLysTyrIleHisProGlnAsnAsnSerIleCysCysThr 20  
 DB 333 GATAGTGTGTGTCCTCCCAAGGAAATATATCCACCTCAAAATAATTCGATTGCTGTACC 492  
 OY 21 LysCysHisLysGlyThrTyrLeuTyrAsnAspCysProGlyProGlyGlnAspThrAsp 40  
 DB 393 AAGTTCCTAAAGAGAACTATTTATTAATGACTGTCTAGGCTCGGGGACGATACGGAC 492  
 OY 41 CysArgGluCysGluSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu 60  
 DB 453 TGTAGGATTTATGAGTGTCTTCTACCTGCTTCAAGAAACCTCAGACACTGCTC 492  
 OY 61 SerCysSerLysCysArgLysGluMetGlyGlnValGluIleSerSerCysThrValAsp 80  
 DB 513 AGTGTCTTAAATGCTTAAAGTAAATGCTTAAAGTAAATGCTTAAAGTAAATGCTTAA 492  
 OY 81 ArgAspThrValCysGlyCysArgLysAsnGlnTyrArgHisTyrTrpSerGluAsnLeu 100  
 DB 573 CGGACACCGT 492  
 OY 101 PheGlnCysPheAsnCysSerLeuCysLeuAsnGlyThrValHisLeuSerCysGlnGlu 120  
 DB 633 TTTCCATCTTCTCAATTCAGATTTCTGTCTTAAATGCTTAAAGTAAATGCTTAAAG 492  
 OY 121 LysGlnAsnThrValCysThrCysHisAlaGlyPhePheLeuArgGluAsnGluCysVal 140  
 DB 693 AAACAGACATTTTATGAGT 492







Percent Similarity: 100.00%  
 Best Local Similarity: 100.00%  
 Query Match: 100.00%  
 DB: 13  
 Gaps: 0

US 09 882-735 2 (1-161) x AAQ20973 (1-2062)

QY 1 AspSerValCysProGlnGlyLysTyrIleHisProGlnAsnAsnSerIleCysCysThr 20  
 DB 275 GATAGTGTGTGTCCTCCCAAGGAAATATATCCACCTCATAAATAATTCGATTTCGTGACC 334  
 QY 21 LysCysHisLysGlyThrTyrLeuTyrAsnAspCysProGlyProGlyGlnAspThrAsp 40  
 DB 335 AAGTGTCCCAAGGAAACCTACTTGTACAAATGACTGTCCAGGCGCGGAGGATACGGAC 394  
 QY 41 CysArgGluCysGluSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu 60  
 DB 395 TGCAGGAGTGTGAGAGGAGTGTTCACCGCTTCAGAAACCCACCTCAGACACTGCCTC 454  
 QY 61 SerCysSerLysCysArgGlyGluMetGlyGlnValGluIleSerSerCysThrValAsp 80  
 DB 455 AGCTGCTCCAAATGCGGAAAGGAAATGGTCAGGTGGAGATCTCTCTTGCACAGTGGAC 514  
 QY 81 ArgAspThrValCysGlyCysArgLysAsnGlnTyrArgHisTyrTrpSerGluAsnLeu 100  
 DB 515 GGTGACACCGTGTGTGTGTCAGGAAAGCAACAGTACCGGCATTATTGGAGTGAACCTT 574  
 QY 101 PheGlnCysPheAsnCysSerLeuCysLeuAsnGlyThrValHisLeuSerCysGlnGlu 120  
 DB 575 TTCCAGTGTTCATTTGATGAGCTTGTCTCAATGGGACCGTGCACCTCTCTGCGCAGGAG 634  
 QY 121 LysGlnAsnThrValCysThrCysHisAlaGlyPhePheLeuArgGluAsnGluCysVal 140  
 DB 635 AAACAGAACACCGTGTGTGTGTCAGGAAAGCAACAGTACCGGCATTATTGGAGTGAACCTT 694  
 QY 141 SerCysSerAsnCysLysLysSerLeuGluCysThrLysLeuCysLeuProGlnIleGlu 160  
 DB 695 TCTCTTATATTAATTTTAAAGAAAGGCTGTGAGTGCAGGAAATGTGTGCTTACCCAGATTGAG 754  
 QY 161 Asn 161  
 DB 755 AAT 757

RESULT 11  
 AAQ24440  
 ID AAQ24440 standard; DNA, 2062 BP.

XX AC AAQ24440;

DT 05 NOV-1992 (first entry)

XX DE Encodes TNF-alpha 55kd receptor.

XX KW tumour necrosis factor alpha; extracellular binding domain;  
 KW treatment; pulmonary diseases; septic shock; HIV infection; AIDS;  
 KW malaria; viral meningitis; graft versus host disease;  
 KW autoimmune disease; rheumatoid arthritis.

XX OS Homo sapiens.

XX PH Key Location/Qualifiers  
 FT CTS 156..1517

FT mat\_peptide /product= human TNF-alpha  
 1265..1267

FT /tag= b

FT /note= "3"

FT mat\_peptide 1265..1267

FT /tag= c

FT /codon= seq "TGG", aa Thr  
 1258..1260

FT mat\_peptide /tag= d

FT /codon= Seq "AAG", aa:Leu

FT mat\_peptide 1433..1435  
 FT /tag= e  
 FT /codon= Seq "GAC", aa:Asn  
 FT sig\_peptide 156..274  
 FT /tag= f  
 XX  
 FN W09207076-A.  
 XX  
 XX 30-APR-1992.  
 XX  
 PF 18-OCT-1991; 91WO-GB01826.  
 XX  
 PR 18-OCT-1990; 90GB-0022648.  
 XX  
 PA (CHAR-) CHARING CROSS SUNLEY RES CENT.  
 XX  
 PI Brennan PM, Feldmann M, Gray PW, Turner MJC;  
 XX  
 DR WPI; 1992-167156/20.  
 DP P-PSDB; AAP24000.  
 XX  
 PT New polypeptide capable of binding human TNF alpha - comprises  
 PT first three cysteine-rich subdomains of TNF alpha receptor for  
 PT treating autoimmune disease, septic shock, HIV etc.  
 XX  
 FS Claim 4; Fig 1; 43pp; English.

This sequence encodes human TNF-alpha 55kd receptor. A placenta cDNA library in gtl0 was screened with probe AAQ29236. Ten hybridising clones were plaque purified and cDNA size determined by PAGE against an Eco RI digested phage DNA. The inserts of two cDNA clones were then sequenced. The coding region of the majority of the human TNF alpha 55kd receptor was isolated as an EcoRI fragment encoding 174 amino acids, and cloned into a mammalian cell expression vector, resulting in pTNFR. A derivative of the TNF-alpha receptor was produced by engineering a termination codon just prior to the transmembrane domain. PCR with primers AAQ29237,8 generated a 300bp restriction fragment which was cloned into pTNFR, giving pTNFRcd. DNA sequencing confirmed this contained the designed DNA sequence. The TNF-alpha receptor expression plasmids were then transfected into monkey COS-7 cells.

CC See also AAQ24440-51, AAR24000, AAR24080-84, AAR27585, AAQ29236-8

SQ Sequence 2062 BP, 429 A, 618 C, 572 G, 443 T; 0 other;

Alignment Scores:

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 Score: 941.00 Matches: 161  
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US 09-882-735 2 (1-161) x AAQ24440 (1-2062)

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QY 21 LysCysHisLysGlyThrTyrLeuTyrAsnAspCysProGlyProGlyGlnAspThrAsp 40

DB 335 AAGTGTCCCAAGGAAACCTACTTGTACAAATGACTGTCCAGGCGCGGAGGATACGGAC 494

QY 41 CysArgGluCysGluSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu 60

DB 395 TGCAGGAGTGTGAGAGGAGTGTTCACCGCTTCAGAAACCCACCTCAGACACTGCCTC 454

QY 61 SerCysSerLysCysArgLysGluMetGlyGlnValGluIleSerSerCysThrValAsp 80

DB 455 AGCTGCTCCAAATGCGGAAAGGAAATGGTCAGGTGGAGATCTCTCTTGCACAGTGGAC 514

QY 81 ArgAspThrValCysGlyCysArgLysAsnGlnTyrArgHisTyrTrpSerGluAsnLeu 100

DB 515 GGTGACACCGTGTGTGTGTCAGGAAAGCAACAGTACCGGCATTATTGGAGTGAACCTT 574

QY 101 PheGlnCysPheAsnCysSerLeuCysLeuAsnGlyThrValHisLeuSerCysGlnGlu 120

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QY 121 LysGlnAsnThrValCysThrCysHisAlaGlyPhePheLeuArgGluAsnGluCysVal 140

DB 635 AAACAGAACACCGTGTGTGTGTCAGGAAAGCAACAGTACCGGCATTATTGGAGTGAACCTT 694

QY 141 SerCysSerAsnCysLysLysSerLeuGluCysThrLysLeuCysLeuProGlnIleGlu 160

DB 695 TCTCTTATATTAATTTTAAAGAAAGGCTGTGAGTGCAGGAAATGTGTGCTTACCCAGATTGAG 754









GenCore version 5.1.3  
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(without alignments)

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Perfect score: 941

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Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DR seq length: 0

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Post processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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2	941	100.0	1301	4	US-08-804-166-7	Sequence 7, Appli
3	941	100.0	1301	4	US-08-910-991-7	Sequence 7, Appli
4	941	100.0	1478	4	US-09-149-922-6	Sequence 6, Appli
5	941	100.0	2062	2	US-08-050-319B-24	Sequence 24, Appli
6	941	100.0	2062	2	US-08-465-982-24	Sequence 24, Appli
7	941	100.0	2161	3	US-09-106-038A-1	Sequence 1, Appli
8	941	100.0	2161	4	US-09-505-250-3	Sequence 3, Appli
9	941	100.0	2175	1	US-08-301-668-1	Sequence 1, Appli
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11	941	100.0	2175	1	US-08-126-016-1	Sequence 1, Appli
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#### ALIGNMENTS

RESULT 1  
US-09-326-394-1  
: Sequence 1, Application US/09326394  
: Patent No. 6306820  
: GENERAL INFORMATION:  
: APPLICANT: Bendelle, Alison M.  
: APPLICANT: Sennello, Regina M.  
: APPLICANT: Edwards, Carl K.  
: TITLE OF INVENTION: COMBINATION THERAPY USING A TIE BINDING  
: TITLE OF INVENTION: PROTEIN FOR TREATING THE MEDIATED DISEASES  
: NUMBER OF SEQUENCES: 4  
: CORRESPONDENCE ADDRESS:  
: ADDRESSEE: Amgen Inc.  
: STREET: 1840 DeHavilland Drive  
: CITY: Thousand Oaks  
: STATE: CA  
: COUNTRY: US  
: ZIP: 91320-1789  
: COMPUTER READABLE FORM:  
: MEDIUM TYPE: Floppy disk  
: COMPUTER: IBM PC compatible  
: OPERATING SYSTEM: PC-DOS/MS-DOS  
: SOFTWARE: Patent In Release #1 0, Version #1 30  
: CURRENT APPLICATION DATA:  
: APPLICATION NUMBER: US/09/326,394  
: FILING DATE: 08-DEC-1997  
: CLASSIFICATION:  
: PRIOR APPLICATION DATA:  
: APPLICATION NUMBER: US 60/030,587  
: FILING DATE: 06-DEC-1996  
: PRIOR APPLICATION DATA:  
: APPLICATION NUMBER: US 60/036,355  
: FILING DATE: 23 JAN-1997  
: PRIOR APPLICATION DATA:  
: APPLICATION NUMBER: US 60/039,315  
: FILING DATE: 07-FEB-1997

```

1 PRIOR APPLICATION DATA: US 60/052,023
2 APPLICATION NUMBER: 09-JUL-1997
3 FILING DATE: 09-JUL-1997
4 ATTORNEY/AGENT INFORMATION:
5 NAME: ZINDRICK, THOMAS K.
6 FIRST/STATION NUMBER: 32,185
7 REFERENCE/DOCKET NUMBER: A-430D
8 INFORMATION FOR SEQ ID NO. 1:
9 SEQUENCE CHARACTERISTICS:
10 LENGTH: 483 base pairs
11 TYPE: nucleic acid
12 STRANDEDNESS: unknown
13 TOPOLOGY: unknown
14 MOLECULE TYPE: cDNA
15 FEATURE:
16 NAME/KEY: CDS
17 LOCATION: 1..483
18 US-09-326-394-1
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20 Alignment Scores:
21 Pred. NO.: 1,17e-93 Length: 483
22 Score: 941.00 Matches: 161
23 Percent Similarity: 100.00% Conservative: 0
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57 RESULT 2
58 US-08-804-166-7
59 Sequence 7, Application US/08804166
60 Patent No. 6193972
61 GENERAL INFORMATION:
62 APPLICANT: Campbell, Robert K.
63 APPLICANT: Jamson, Bradford A.
64 APPLICANT: Chappel, Scott C.

```

```

1 TITLE OF INVENTION: HYBRID PROTEINS
2 NUMBER OF SEQUENCES: 22
3 CORRESPONDENCE ADDRESS:
4 ADDRESSEE: BROWDY AND NEIMARK
5 STREET: 419 Seventh Street N.W., Ste. 300
6 City: Washington
7 STATE: D.C.
8 COUNTRY: USA
9 ZIP: 22207
10
11 COMPUTER READABLE FORM:
12 MEDIUM TYPE: Floppy disk
13 COMPUTER: IBM PC compatible
14 OPERATING SYSTEM: PC-DOS/MS-DOS
15 SOFTWARE: PatentIn Release #1.0, Version #1.30
16 CURRENT APPLICATION DATA:
17 APPLICATION NUMBER: US/08/804,166
18 FILING DATE:
19 CLASSIFICATION:
20 PRIOR APPLICATION DATA:
21 APPLICATION NUMBER: 60/011,936
22 FILING DATE: 20 February 1996
23 CLASSIFICATION:
24 ATTORNEY/AGENT INFORMATION:
25 NAME: Browdy, Roger L.
26 REGISTRATION NUMBER: 25,618
27 REFERENCE/DOCKET NUMBER: CAMPBELL=2A
28 TELECOMMUNICATION INFORMATION:
29 TELEPHONE: (202) 628-5197
30 TELEFAX: (202) 737-3528
31 INFORMATION FOR SEQ ID NO: 7:
32 SEQUENCE CHARACTERISTICS:
33 LENGTH: 1301 base pairs
34 TYPE: nucleic acid
35 STRANDEDNESS: single
36 TOPOLOGY: linear
37 MOLECULE TYPE: cDNA
38 FEATURE:
39 NAME/KEY: CDS
40 LOCATION: 279..1287
41 US-08-804-166-7
42
43 Alignment Scores:
44 Pred. No.: 4,71e-93 Length: 1301
45 Score: 941.00 Matches: 161
46 Percent Similarity: 100.00% Conservative: 0
47 Best Local Similarity: 100.00% Mismatches: 0
48 Query Match: 100.00% Indels: 0
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58 Db 465 TGCACGAGCTGTGAAGACGAGCTCTCCCTTCACCCGCTTCAGAAACACACTGACACTGCTTC 524
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## RESULT 3

US-08-910-991-7  
; Sequence 7, Application US/08910991  
; Patent No. 6194177  
; GENERAL INFORMATION:  
; APPLICANT: Campbell, Robert K.  
; APPLICANT: Jameson, Bradford A.  
; APPLICANT: Chappel, Scott C.  
; TITLE OF INVENTION: HYBRID PROTEINS  
; NUMBER OF SEQUENCES: 22  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK  
; STREET: 419 Seventh Street N W , Ste 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 22207  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/910,991  
; FILING DATE:  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/804,166  
; FILING DATE: 20 February 1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/011,936  
; FILING DATE: 20 February 1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: YUN, Allen C.  
; REGISTRATION NUMBER: 37,971  
; REFERENCE/CO-PAT NUMBER: CAMPBELL 2B  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 628 5197  
; TELEFAX: (202) 737 3528  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1101 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 279..1287

US-08-910-991-7

Alignment Scores:  
Pred. No.: 4.71e-93 Length: 1301  
Score: 941.00 Matches: 161  
Percent Similarity: 100.00% Conservative: 0  
Best local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
Dd: 4 Gaps: 0

US-09-882-735-2 (1-161) x US-08-910-991-7 (1-1301)  
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Dd 345 GATAGTGTGTGTCCTCCCAAGGAAAATATATGACGCTTCAAAAATAATTGATTGAGTGA 404  
Qy 21 LysCysHisLysGlyThrTyrLeuTyrAsnAspCysProGlyGlnAspThrAsp 40  
Dd 405 AAGTCCACCAAAAGGAACTTACTTTTAATATATGATGCTGCTGCTGCTGCTGCTGCTG 464  
Qy 41 CysArgGluCysGluSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysGlu 60  
Dd 465 TSCAGGAGTGTGAGAGCGGCTCTTCCACGCTTCCAGAAAACCCCTCAATCTGATGTC 624  
Qy 61 SerCysSerLysCysArgLysGluMetGlyGlnValGluIleSerSerCysThrValAsp 80  
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Qy 81 ArgAspThrValCysGlyCysArgLysAsnGlnTyrArgHisTyrTrpSerGluAsnLeu 100  
Dd 585 CGGACACACCGTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 644  
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Dd 825 AAT 827

## RESULT 4

US-09-149-922-6  
; Sequence 6, Application US/09149922A  
; Patent No. 6265174  
; GENERAL INFORMATION:  
; APPLICANT: Menzel, Rolf  
; APPLICANT: Hsing, Weihong  
; APPLICANT: Taggart, Pamela  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR IDENTIFYING AND MODULATING  
; TITLE OF INVENTION: PROTEIN-PROTEIN INTERACTIONS  
; FILE REFERENCE: 9366-006  
; CURRENT APPLICATION NUMBER: US/09/149,922A  
; CURRENT FILING DATE: 1998-09-09  
; EARLIER APPLICATION NUMBER: 60/064,058  
; EARLIER FILING DATE: 1997-11-03  
; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO 6  
; LENGTH: 1478  
; TYPE: DNA  
; ORGANISM: Escherichia coli  
; FEATURE:  
; NAME/KEY: modified\_base  
; LOCATION: 58  
; OTHER INFORMATION: n=a, c, g, or t  
; FEATURE:  
; NAME/KEY: modified\_base  
; LOCATION: 105  
; OTHER INFORMATION: n=a, c, g, or t  
; OTHER INFORMATION: n=a, c, g, or t

US-09-149-922-6

Alignment Scores:  
Pred. No.: 5.63e-93 Length: 1478  
Score: 941.00 Matches: 161  
Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 2  
DB: 4 Gaps: 0

US-09-882-735-2 (1-161) X US-09-149-922-6 (1-1478)

QY 1 AspSerValCysProGlnGlyLysThrIleHisProGlnAsnAsnSerIleCysCysThr 20  
DB 941 GATGAGTGTGTCCCAAGAAATATTCACCCCTCAAAATATTCGATTGGTGTAC 1000  
QY 21 LysCysHisSerGlyThrTyLeuTyAsnAspCysProGlyProGlyGlnAspThrAsp 40  
DB 1001 AAATGTCATAAAGAACCTATCTTGTACATATCTTCCAGGCGCGGCGAGATCGGAC 1060  
QY 41 CysArgGluCysGlySerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu 60  
DB 1061 TCCAGGCGGAGTGTGAGAGCGGCTTCCTTCACCGCTTCAGAAACCCACGACACTGCTTC 1120  
QY 61 SerCysSerLysCysArgGlyGluMetGlyGlnValGluIleSerSerCysThrValAsp 80  
DB 1121 AATGTCATAAAGAACCTATCTTGTACATATCTTCCAGGCGGAGATCGGAC 1180  
QY 91 ArgAspThrValCysGlyCysArgGlyAsnGlnIleTyArgHisTyTrpSerGluAsnLeu 100  
DB 1181 GAGGAGTGTGTCCCAAGAAATATTCACCCCTCAAAATATTCGATTGGTGTAC 1240  
QY 121 PheGlnCysPheAsnCysSerLeuCysLeuAsnGlyThrValHisLeuSerCysGlnGlu 120  
DB 1241 TCCAGGCGGAGTGTGAGAGCGGCTTCCTTCACCGCTTCAGAAACCCACGACACTGCTTC 1300  
QY 121 LysGlnAsnThrValCysThrCysHisAlaGlyPhePheLeuArgGluAsnGluCysVal 140  
DB 1301 AAATGTCATAAAGAACCTATCTTGTACATATCTTCCAGGCGGAGATCGGAC 1360  
QY 141 SerCysSerAsnCysLysSerLeuGluCysThrLysLeuCysLeuProGlnIleGlu 160  
DB 1361 TCCAGGCGGAGTGTGAGAGCGGCTTCCTTCACCGCTTCAGAAACCCACGACACTGCTTC 1420  
QY 161 Asn 161  
DB 1421 AAT 1423

RESULT 5  
US-08-050-319B-24  
Sequence 24 Application US/08050319B  
Patent No. 5633145  
GENERAL INFORMATION:  
APPLICANT: M. Feldmann, P.W. Gray,  
APPLICANT: M.J.C. Turner, F.M. Brennan  
TITLE OF INVENTION: Modified human TNFalpha (Tumor  
Necrosis Factor alpha) Receptor  
NUMBER OF SEQUENCES: 57  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Reed & Robbins  
STREET: 635 Bryant Street  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94301  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/050,319B  
FILING DATE: 10-May-1993  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Robbins, Roberta L.  
REGISTRATION NUMBER: 33,208  
REFERENCE/KEY NUMBER: 5150-0030  
TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 617-8999  
TELEFAX: (415) 327-3231  
INFORMATION FOR SEQ ID NO: 24:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2062 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA to mRNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 155..1519  
US-08-050-319B-24

#### Alignment Scores:

Pred. No.: 8,98E-93 Length: 2062  
Score: 941.00 Matches: 161  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
Gaps: 0

US-09-882-735-2 (1-161) X US-08-050-319B-24 (1-2062)

QY 1 AspSerValCysProGlnGlyLysThrIleHisProGlnAsnAsnSerIleCysCysThr 20  
DB 275 GATGAGTGTGTCCCAAGAAATATTCACCCCTCAAAATATTCGATTGGTGTAC 334  
QY 21 LysCysHisSerGlyThrTyLeuTyAsnAspCysProGlyProGlyGlnAspThrAsp 40  
DB 335 AAGTGCCACAAAGAACCTATCTTGTACATATCTTCCAGGCGCGGCGAGATCGGAC 394  
QY 41 CysArgGluCysGlySerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu 60  
DB 395 TGCAGGAGTGTGAGAGCGGCTTCCTTCACCGCTTCAGAAACCCACGACACTGCTTC 454  
QY 61 SerCysSerLysCysArgGlyGluMetGlyGlnValGluIleSerSerCysThrValAsp 80  
DB 455 AGCTGCTCCAAATCCGAAAGGAAATGGGTCAAGTGAATCTCTTCTTGCACAGTGAGC 514  
QY 81 ArgAspThrValCysGlyCysArgGlyAsnGlnIleTyArgHisTyTrpSerGluAsnLeu 100  
DB 515 CGGACACCGGTGTGTGCTGCAGAGAACACAGTACCGGCATTATGAGTGAACCACTT 574  
QY 101 PheGlnCysPheAsnCysSerLeuCysLeuAsnGlyThrValHisLeuSerCysGlnGlu 120  
DB 575 TCCAGGCGGAGTGTGAGAGCGGCTTCCTTCACCGCTTCAGAAACCCACGACACTGCTTC 634  
QY 121 LysGlnAsnThrValCysThrCysHisAlaGlyPhePheLeuArgGluAsnGluCysVal 140  
DB 635 AAATGTCATAAAGAACCTATCTTGTACATATCTTCCAGGCGGAGATCGGAC 694  
QY 141 SerCysSerAsnCysLysSerLeuGluCysThrLysLeuCysLeuProGlnIleGlu 160  
DB 695 TCCAGGCGGAGTGTGAGAGCGGCTTCCTTCACCGCTTCAGAAACCCACGACACTGCTTC 754  
QY 161 Asn 161  
DB 755 AAT 757

RESULT 6  
US-08-465-982-24  
Sequence 24 Application US/08465982  
Patent No. 563786  
GENERAL INFORMATION:  
APPLICANT: M. Feldmann, P.W. Gray,  
APPLICANT: M.J.C. Turner, F.M. Brennan  
TITLE OF INVENTION: Modified human TNFalpha (Tumor  
Necrosis Factor alpha) Receptor  
NUMBER OF SEQUENCES: 57  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Reed & Robbins  
STREET: 635 Bryant Street







Query Match: 100.00% Indels: 0  
DB: 1 Gaps: 0  
US 09-882-735-2 (1-161) x US 08-837-941-1 (1-2175)  
QY 1 AspSerValCysProGlnGlyTyrIleHisProGlnAsnSerIleCysCysThr 20  
DB 376 CATAGTGTGTCTCCCAAGGAAAATATATCCACCTCAAAATAATTCGATTTCGTGAC 435  
QY 21 LysCysHisIleGlyThrTyrLeuTyrAsnAspCysProGlyProGlyGlnAspThr 40  
DB 436 AAGTGTCTCAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGAGGATACGGAC 495  
QY 41 CysArgGluCysGluSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu 60  
DB 496 TGCAGGAGTCTGTACAGTGGCTCTTACCGCTTCAGAAACACCTCCAGACACTGCCCTC 555  
QY 61 SerCysSerIleCysArgGluMetGlyGlnValGluIleSerSerCysThrValAsp 80  
DB 556 AGTGTCTCAAAATGCAAGGAAAATATATCCACCTCAAAATAATTCGATTTCGTGAC 615  
QY 81 ArgAspThrValCysGlyCysArgLysAsnGlnTyrArgHisTyrTrpSerGluAsnLeu 100  
DB 616 CGGACACCGGT 675  
QY 101 PheGlnCysPheAsnCysSerLeuCysLeuAsnGlyThrValHisLeuSerCysGlnGlu 120  
DB 676 TTCCAGTGTCTTCAATTCAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 735  
QY 121 LysGlnAsnThrValCysThrCysHisAlaGlyPhePheLeuArgGluCysVal 140  
DB 736 AAAACAAATGCTGT 795  
QY 141 SerCysSerAsnCysLysLysSerLeuGluCysThrLysLeuCysLeuProGlnIleGlu 160  
DB 796 TCTCTGTAGTAACTTAAAGAAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 855  
QY 161 Asn 161  
DB 856 AAT 858  
RESULT 10  
US 08-837-941-1  
; Sequence 1, Application US/08837941  
; Patent No. 5766917  
; GENERAL INFORMATION:  
; APPLICANT: WALLACH, David  
; APPLICANT: BAKERFISCH, Cord  
; APPLICANT: VAPLOMEY, Eugene  
; APPLICANT: BATKIN, Michael  
; TITLE OF INVENTION: MOLECULES INFLUENCING THE SHEDDING OF  
; TITLE OF INVENTION: THE TNF RECEPTORS, THEIR PREPARATION AND THEIR USE  
; NUMBER OF SEQUENCES: 42  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK  
; STREET: 419 Seventh Street, N.W., Suite 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/837,941  
; FILING DATE: 28 APR-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/321,668  
; FILING DATE: 12 OCT 1994  
; APPLICATION NUMBER: IL 107268

FILING DATE: 12-OCT-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: BROWDY, Roger L.  
REGISTRATION NUMBER: 25,618  
REFERENCE/DOCKET NUMBER: WALLACH=13  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
TELEX: 248633  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2175 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 256..1620  
US-08-837-941-1  
Alignment Scores:  
Pred. No.: 9,67e-93 Length: 2175  
Score: 941.00 Matches: 161  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 1 Gaps: 0  
US-09-882-735-2 (1-161) x US-08-837-941-1 (1-2175)  
QY 1 AspSerValCysProGlnGlyTyrIleHisProGlnAsnSerIleCysCysThr 20  
DB 376 CATAGTGTGTCTCCCAAGGAAAATATATCCACCTCAAAATAATTCGATTTCGTGAC 435  
QY 21 LysCysHisIleGlyThrTyrLeuTyrAsnAspCysProGlyProGlyGlnAspThr 40  
DB 436 AAGTGTCTCAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGAGGATACGGAC 495  
QY 41 CysArgGluCysGluSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu 60  
DB 496 TGCAGGAGTCTGTACAGTGGCTCTTACCGCTTCAGAAACACCTCCAGACACTGCCCTC 555  
QY 61 SerCysSerIleCysArgGluMetGlyGlnValGluIleSerSerCysThrValAsp 80  
DB 556 AGTGTCTCAAAATGCAAGGAAAATATATCCACCTCAAAATAATTCGATTTCGTGAC 615  
QY 81 ArgAspThrValCysGlyCysArgLysAsnGlnTyrArgHisTyrTrpSerGluAsnLeu 100  
DB 616 CGGACACCGGT 675  
QY 101 PheGlnCysPheAsnCysSerLeuCysLeuAsnGlyThrValHisLeuSerCysGlnGlu 120  
DB 676 TTCCAGTGTCTTCAATTCAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 735  
QY 121 LysGlnAsnThrValCysThrCysHisAlaGlyPhePheLeuArgGluCysVal 140  
DB 736 AAAACAAATGCTGT 795  
QY 141 SerCysSerAsnCysLysLysSerLeuGluCysThrLysLeuCysLeuProGlnIleGlu 160  
DB 796 TCTCTGTAGTAACTTAAAGAAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 855  
QY 161 Asn 161  
DB 856 AAT 858  
RESULT 11  
US-08-126-016-1  
; Sequence 1, Application US/08126016  
; Patent No. 5811261  
; GENERAL INFORMATION:  
; APPLICANT: WALLACH, DAVID





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1 COMPUTER READABLE FORM:
2 MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
3 COMPUTER: IBM PC compatible
4 OPERATING SYSTEM: PC-DOS/MS-DOS
5 SOFTWARE: patin (Genentech)
6 CURRENT APPLICATION DATA:
7 APPLICATION NUMBER: P01/U0345/00576
8 FILING DATE:
9 CLASSIFICATION:
10 PRIOR APPLICATION DATA:
11 AFFILIATION NUMBER: 08/296740
12 FILING DATE: 05-AUG-1994
13 AGENCY/AGENCY INFORMATION:
14 NAME: lee, Wendy M.
15 REGISTRATION NUMBER: 00,000
16 REFERENCE/PRIORITY NUMBER: 704P07
17 TELECOMMUNICATION INFORMATION:
18 TELEPHONE: 415/225-1994
19 TELEFAX: 415/225-2931
20 TELEX: 910/337-7168
21 INFORMATION FOR SEQ ID NO. 2:
22 SEQUENCE CHARACTERISTICS:
23 LENGTH: 6689 bases
24 TYPE: nucleic acid
25 STRANDEDNESS: double
26 TOPOLOGY: linear
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Alignment Scores:
Pred: NCBI      4.87e+92      Length: 6889
Score:          941.00      Matches: 161
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:    100.00%      Indels: 0
DB:             5          Gaps: 0

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[illegible]

RESULT 15  
US-08-627-151A-6  
; Sequence 6, Application US/08627151A

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1  GENERAL INFORMATION:
2  APPLICANT: SPINELLA, Dominic
3  APPLICANT: BECHERER, Kathleen
4  APPLICANT: BROWN, Steven
5  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
6  TITRE OF INVENTION: SCREENING DRUG LIBRARIES
7  NUMBER OF SEQUENCES: 19
8

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ADDRESSEE: Gen-Probe Incorporated  
STREET: 10210 Genetic Center Drive  
CITY: San Diego  
STATE: CA  
COUNTRY: USA

```

1  COMPUTER READABLE FORM:
2  MEDIUM TYPE: Diskette
3  COMPUTER: IBM Compatible
4  OPERATING SYSTEM: DOS
5  SOFTWARE: PASTESQ for Windows Version 2.0
6  CURRENT APPLICATION DATA:
7  APPLICATION NUMBER: US/08/657,151A
8  FILING DATE: 03-APR-1996

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1 FILING DATE:  
2 ATTORNEY/AGENT INFORMATION  
3 NAME: FISHER, CARLOS A  
4 REGISTRATION NUMBER: 36,510  
5 REFERENCE/DOCKET NUMBER: C01016  
6 TELECOMMUNICATION INFORMATION:  
7 TELEPHONE: 619-410-8926  
8 TELEFAX: 619-410-8928

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; INFORMATION FOR SEQ ID NO: 6
;
; SEQUENCE CHARACTERISTICS:
;
; LENGTH: 6896 base pairs
;
; TYPE: nucleic acid
;
; STRANDEDNESS: single
;
; TOPOLOGY: linear
;

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Alignment Scores:	
Pred. No.:	4,88e-92
Score:	941.00
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	100.00%
DB:	2
Length:	6896
Matches:	161
Conservative:	0
Mismatches:	0
Indels:	0
Gaps:	0

QY	1	AspSerValysproGlnGlyIysThrIleHisproGlnAsnAsnSerTlleCysCysThr	20
QY	21	LysCysHisIysGlyThrTyrLeuTyrAsnAspCysProGlyProGlyGlnAspThrAsp	40
Db	1115	AAAGGCCACAAAGAAACCTACTTGTACATGACTGTCCAGGCCGGGAGAGATACGAC	1174
QY	41	CysHISGluCysGluSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu	60
Db	1175	TGCAGGAGAGTGCAGAGCGGCTCTTCACCCCTTCAGAAACACACCTCAGACACTGCTC	1234
QY	61	SerCysSerIysCysArgIysGluMetGlyGlnValGluIleSerSerCysThrValAsp	80
Db	1235	AGCTGCTCCAAATGCCGAAGAGAAATGGGTATGGGTAGGAGATCTTCTTCTTGACACAGTGAC	1294



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GenCore version 5.1.3  
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OM protein nucleic search, using frame\_plus\_p2n model

Run on: January 6, 2003, 04:00:40 ; Search time 273 Seconds  
(without alignments)

255.067 Million cell updates/sec

Title: US-09-882-735-2

Perfect score: 941

Sequence: 1 DSVCPQKRYHPQNSICCT . . . . CSNCKSLECKLCPQIEN 161

Scoring table: RLOSUM62

Xgapop 10 0 0 Xgapext 0 5

Ygapop 10 0 0 Ygapext 0 5

Delop 6 0 0 Delapext 7 0

Delop 6 0 0 Delapext 7 0

Searched: 381593 seqs, 216252194 residues

Total number of hits satisfying chosen parameters: 763186

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

MODEL=frame\_p2n.model -DEV=xlh

Q=/cqn2\_1/USPTO\_SPEC/US0982735/tunat\_03012003\_074143\_17088/app\_query.fasta\_1.327

DB=Published Applications NA -QFMT=fastap -SUFFIX=rnpb -MINMATCH=0.1

-LCOPTCL=0 -LCOPEXT=0 -INITTS=bits -START=1 -END=1 -MATRIX=blomsum62

TRANS=humand4 codi -LIST=45 -DOCCALIGN=200 -THP SCOPE=PCT -THP MAX=100

THR MIN=0 ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext HEAPSIZ=500 MINLEN=0

MAXLEN 200000000 USER=US0982735 -QFMT 1 1 24 -runat 03012003\_074143\_17088

NCTPU=6 -ICPU=3 -NO\_XLPUX -NO\_WMAP -LAPGQUERY -NEG\_SCORES=0 -WAIT -LONGLOG

DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -PGAPOP=6

MAPEXT=7 YGAPOP=10 YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Published Applications NA:

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2: /cqn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq:  
3: /cqn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq:  
4: /cqn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq:  
5: /cqn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq:  
6: /cqn2\_6/ptodata/1/pubpna/PCTUS\_PUBCOMB.seq:  
7: /cqn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq:  
8: /cqn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq:  
9: /cqn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq:  
10: /cqn2\_6/ptodata/1/pubpna/US09\_PTECOMB.seq:  
11: /cqn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq:  
12: /cqn2\_6/ptodata/1/pubpna/US10\_PUBCOMB.seq:  
13: /cqn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq:  
14: /cqn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq:

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	941	100.0	483	9	US-09-898-234-3 Sequence 3, Appl1
2	941	100.0	483	9	US-09-899-429A-3 Sequence 3, Appl1
3	941	100.0	483	9	US-09-792-356-3 Sequence 3, Appl1
4	941	100.0	483	10	US-09-899-422-3 Sequence 3, Appl1

5	941	100.0	483	10	US-09-907-263-1 Sequence 1, Appl1
6	941	100.0	486	9	US-09-899-429A-5 Sequence 5, Appl1
7	941	100.0	516	9	US-09-899-429A-19 Sequence 19, Appl1
8	941	100.0	519	9	US-09-899-429A-15 Sequence 15, Appl1
9	941	100.0	549	9	US-09-899-429A-9 Sequence 9, Appl1
10	941	100.0	578	9	US-09-899-429A-17 Sequence 17, Appl1
11	941	100.0	600	9	US-09-899-429A-11 Sequence 11, Appl1
12	941	100.0	603	9	US-09-899-429A-13 Sequence 13, Appl1
13	941	100.0	633	9	US-09-899-429A-7 Sequence 7, Appl1
14	941	100.0	1301	10	US-09-756-186-7 Sequence 7, Appl1
15	941	100.0	1334	9	US-09-898-234-11 Sequence 11, Appl1
16	941	100.0	1334	9	US-09-792-356-11 Sequence 11, Appl1
17	941	100.0	1334	10	US-09-899-422-11 Sequence 11, Appl1
18	941	100.0	1368	9	US-09-898-234-1 Sequence 1, Appl1
19	941	100.0	1368	9	US-09-899-429A-1 Sequence 1, Appl1
20	941	100.0	1368	9	US-09-792-356-1 Sequence 1, Appl1
21	941	100.0	1368	10	US-09-899-422-1 Sequence 1, Appl1
22	941	100.0	2111	10	US-09-880-157-2360 Sequence 2360, Ap
23	941	100.0	2141	9	US-09-898-234-16 Sequence 16, Appl1
24	941	100.0	2141	9	US-09-899-429A-26 Sequence 26, Appl1
25	941	100.0	2141	9	US-09-792-356-16 Sequence 16, Appl1
26	941	100.0	2141	10	US-09-899-422-16 Sequence 16, Appl1
27	941	100.0	2175	12	US-10-120-397-1 Sequence 1, Appl1
28	931	98.9	1334	9	US-09-899-429A-21 Sequence 21, Appl1
29	928	98.6	1147	10	US-09-756-186-5 Sequence 5, Appl1
30	842.5	89.5	1048	10	US-09-756-186-1 Sequence 1, Appl1
31	837	88.9	1263	10	US-09-756-186-3 Sequence 3, Appl1
32	680	72.3	5870	10	US-09-838-718A-8 Sequence 8, Appl1
33	674.5	71.7	543	10	US-09-970-532-3 Sequence 3, Appl1
34	674.5	71.7	2440	10	US-09-970-532-1 Sequence 1, Appl1
35	669	71.1	2130	10	US-09-917-800A-1601 Sequence 1601, Ap
36	656	69.7	2173	9	US-09-898-234-14 Sequence 14, Appl1
37	656	69.7	2173	9	US-09-899-429A-24 Sequence 24, Appl1
38	656	69.7	2173	9	US-09-792-356-14 Sequence 14, Appl1
39	656	69.7	2173	10	US-09-899-422-14 Sequence 14, Appl1
40	293	31.1	158	9	US-09-898-234-68 Sequence 68, Appl1
41	293	31.1	158	9	US-09-792-356-68 Sequence 68, Appl1
42	293	31.1	158	10	US-09-899-422-68 Sequence 68, Appl1
43	273	29.0	158	9	US-09-899-429A-78 Sequence 78, Appl1
44	255.5	27.2	151	9	US-09-898-234-29 Sequence 29, Appl1
45	255.5	27.2	151	9	US-09-899-429A-30 Sequence 30, Appl1

#### ALIGNMENTS

RESULT 1  
US-09-898-234-3  
; Sequence 3, Application US/09898234  
; Patent No. US20020155112A1  
; GENERAL INFORMATION:  
; APPLICANT: Hauptmann, Rudolph  
; APPLICANT: Himmler, Adolph  
; APPLICANT: Maurer-Fogy, Ingrid  
; APPLICANT: Stratowa, Christian  
; TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for  
; FILE REFERENCE: 98,385-1  
; CURRENT APPLICATION NUMBER: US/09/898,234  
; PRIOR FILING DATE: 2001-07-03  
; PRIOR APPLICATION NUMBER: 09/525,998  
; PRIOR FILING DATE: 2000-03-15  
; PRIOR APPLICATION NUMBER: 08/383,676  
; PRIOR FILING DATE: 1995-02-01  
; PRIOR APPLICATION NUMBER: 08/153,287  
; PRIOR FILING DATE: 1993-11-17  
; PRIOR APPLICATION NUMBER: 07/821,750  
; PRIOR FILING DATE: 1992-01-02  
; PRIOR APPLICATION NUMBER: 07/511,410  
; PRIOR FILING DATE: 1990-04-20  
; NUMBER OF SEQ ID NOS: 87  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 3  
; LENGTH: 483

TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1)..(483)  
US-09-898-234-3

## Alignment Scores:

Pred. No.	Length:	Matches:	Conservative:	Mismatches:	Indels:
3,22e-94	483	161	0	0	0
Score:	941.00				
Percent Similarity:	100.00%				
Best Local Similarity:	100.00%				
Query Match:	100.00%				
DB:	9	Gaps:	0		

US-09-882-735-2 (1-161) x US-09-898-234-3 (1-483)

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Cv 1 AspSerValCysProGlnGlyLysTyrIleHisProGlnAsnAsnSerIleCysCysThr 20
Db 1 GATAGTGTGTGCCCCAAGGAAATATATCCACCTCAAAATATGATTTGCTGTACC 60
Cv 21 LysCysHisLysGlyThrTyrLeuTyrAsnAspCysProGlyProGlyGlnAspThrAsp 40
Db 61 AAGTGTCTAATAAGGAAACCTACTTGTACATATCTTCCAGCCCGGCGGAGATACCGAC 120
Cv 41 CysArgGluCysGlnSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu 60
Db 121 TGAAGGAAATGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 180
Cv 61 SerCysSerLysCysArgLysGlnMetGlyGlnValGlnIleSerSerCysThrValAsp 80
Db 181 AATTGTCTTCAATATGAGGAAATATATATATATATATATATATATATATATATATAT 240
Cv 81 ArgAspThrValCysGlyCysArgLysAsnGlnTyrArgHisTyrTyrSerGluAsnLeu 100
Db 241 CCGGACACCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 300
Cv 101 PheGlnCysPheAsnCysSerLeuCysLeuAsnGlyThrValHisLeuSerCysGlnGlu 120
Db 301 TTCAGTGTCTTCAATATGAGGAAATATATATATATATATATATATATATATATATAT 360
Cv 121 LysGlnAsnThrValCysThrCysHisAlaGlyPhePheLeuArgGlnAsnGluCysVal 140
Db 361 AATCAGGAAACCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 420
Cv 141 SerCysSerAsnCysLysLysSerLeuGluCysThrLysLeuCysLeuProGlnIleGln 160
Db 421 TCCGTACTACTAATGAGGAAATATATATATATATATATATATATATATATATATAT 480
Cv 161 Asn 161
Db 481 AAT 483

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RESULT 2  
US-09-899-429A-3  
Sequence 3, Application US/09899429A  
Parent No. US20020169118A1  
GENERAL INFORMATION:  
APPLICANT: Hauptmann, Rudolph  
APPLICANT: Himmeler, Adolph  
APPLICANT: Maurer-Fogy, Ingrid  
APPLICANT: Stratowa, Christian  
TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for  
TITLE OF INVENTION: Them  
FILE REFERENCE: 98-385-J  
CURRENT APPLICATION NUMBER: US/09/899,429A  
CURRENT FILING DATE: 2001-07-03  
PRIORITY APPLICATION NUMBER: 09/779,356  
PRIORITY FILING DATE: 2000-02-23  
PRIORITY APPLICATION NUMBER: 08/477,639  
PRIORITY FILING DATE: 1995-06-07  
PRIORITY APPLICATION NUMBER: 08/383,676  
PRIORITY FILING DATE: 1995-02-01

PRIOR APPLICATION NUMBER: 08/153,287  
PRIOR FILING DATE: 1993-11-17  
PRIOR APPLICATION NUMBER: 07/821,750  
PRIOR FILING DATE: 1992-01-02  
PRIOR APPLICATION NUMBER: 07/511,430  
PRIOR FILING DATE: 1990-04-20  
NUMBER OF SEQ ID NOS: 97  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO: 3  
LENGTH: 483  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1)..(483)  
US-09-899-429A-3

## Alignment Scores:

Pred. No.	Length:	Matches:	Conservative:	Mismatches:	Indels:
3,22e-94	483	161	0	0	0
Score:	941.00				
Percent Similarity:	100.00%				
Best Local Similarity:	100.00%				
Query Match:	100.00%				
DB:	9	Gaps:	0		

US-09-882-735-2 (1-161) x US-09-899-429A-3 (1-483)

```

Cv 1 AspSerValCysProGlnGlyLysTyrIleHisProGlnAsnAsnSerIleCysCysThr 20
Db 1 GATAGTGTGTGCCCCAAGGAAATATATCCACCTCAAAATATGATTTGCTGTACC 60
Cv 21 LysCysHisLysGlyThrTyrLeuTyrAsnAspCysProGlyProGlyGlnAspThrAsp 40
Db 61 AAGTGTCTAATAAGGAAACCTACTTGTACATATCTTCCAGCCCGGCGGAGATACCGAC 120
Cv 41 CysArgGluCysGlnSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu 60
Db 121 TGAAGGAAATGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 180
Cv 61 SerCysSerLysCysArgLysGlnMetGlyGlnValGlnIleSerSerCysThrValAsp 80
Db 181 AATTGTCTTCAATATGAGGAAATATATATATATATATATATATATATATATATATAT 240
Cv 81 ArgAspThrValCysGlyCysArgLysAsnGlnTyrArgHisTyrTyrSerGluAsnLeu 100
Db 241 CCGGACACCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 300
Cv 101 PheGlnCysPheAsnCysSerLeuCysLeuAsnGlyThrValHisLeuSerCysGlnGlu 120
Db 301 TTCAGTGTCTTCAATATGAGGAAATATATATATATATATATATATATATATATATAT 360
Cv 121 LysGlnAsnThrValCysThrCysHisAlaGlyPhePheLeuArgGlnAsnGluCysVal 140
Db 361 AATCAGGAAACCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 420
Cv 141 SerCysSerAsnCysLysLysSerLeuGluCysThrLysLeuCysLeuProGlnIleGln 160
Db 421 TCCGTACTACTAATGAGGAAATATATATATATATATATATATATATATATATATAT 480
Cv 161 Asn 161
Db 481 AAT 483

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RESULT 3  
US-09-792-356-3  
Sequence 3, Application US/09792356  
Publication No. US20020183485A1  
GENERAL INFORMATION:  
APPLICANT: Hauptmann, Rudolph  
APPLICANT: Himmeler, Adolph  
APPLICANT: Maurer-Fogy, Ingrid  
APPLICANT: Stratowa, Christian  
TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for





D6	421	TGCTGTATTAACCTTAAAGAAAAAGTTGGTAGTGAGATTTCGCTAACCCCAATGAG	480
Cy	161	Asn	161
D6	481	AAT	483







DB 146 AADAGCCAAAGGAACTATTCTATACATCTCCACGCGCGGACAGGATACCGAC 207  
 QY 41 CysArgGluCysGlnSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu 60  
 DB 208 TCGAGGACATCTGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 267  
 QY 41 SerCysSerLysCysArgLysGlnMetGlyGlnValHisIleSerSerCysThrValAsp 80  
 DB 269 AATCTCTGCAATCTCCGAAAGGAAATGCGATCTGACGATCTCTCTTGGACAGTGAC 327  
 QY 89 AAGAGCTTAAAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 100  
 DB 328 CCGGAAATCTGAG 387  
 QY 101 PheGlnCysPheAsnGlySerLeuGlnGlyThrValHisLeuSerCysGlnGlu 120  
 DB 448 TCGAGGACATCTGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 447  
 QY 121 LysGlnAsnThrValCysThrCysHisAlaGlyPhePheLeuArgGluAsnGluCysVal 140  
 DB 444 AAAAAGAAAG 507  
 QY 141 SerCysSerLysCysArgLysGlnMetGlyGlnValHisIleSerSerCysThrValAsp 160  
 DB 508 TCGAGGACATCTGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 567  
 QY 161 Asn 161  
 DB 568 AAT 570  
 RESULT 12  
 US-09-899-429A-13  
 / Sequence 13, Application US/09899429A  
 / Patent No. US20020169118A1  
 / GENERAL INFORMATION:  
 / APPLICANT: Hauptmann, Rudolph  
 / APPLICANT: Hammler, Adolph  
 / APPLICANT: Maurer-Fogy, Ingrid  
 / APPLICANT: Stratowa, Christian  
 / TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for  
 / FILE REFERENCE: 98-385-J  
 / CURRENT APPLICATION NUMBER: US/09/899-429A  
 / CURRENT FILING DATE: 2001-07-03  
 / PRIOR APPLICATION NUMBER: 08/477,636  
 / PRIOR FILING DATE: 1995-06-07  
 / PRIOR APPLICATION NUMBER: 08/383,676  
 / PRIOR FILING DATE: 1995-02-01  
 / PRIOR APPLICATION NUMBER: 08/153,287  
 / PRIOR FILING DATE: 1993-11-17  
 / PRIOR APPLICATION NUMBER: 07/821,750  
 / PRIOR FILING DATE: 1992-01-02  
 / PRIOR APPLICATION NUMBER: 07/511,430  
 / PRIOR FILING DATE: 1990-04-20  
 / NUMBER OF SEQ ID NOS: 97  
 / SOFTWARE: PatentIn Ver. 2.0  
 / SEQ ID NO 13  
 / LENGTH: 603  
 / TYPE: DNA  
 / ORGANISM: Artificial Sequence  
 / FEATURE:  
 / OTHER INFORMATION: Description of Artificial Sequence: recombinant  
 / OTHER INFORMATION: TNF-RP sequence  
 / NAME/KEY: CDS  
 / LOCATION: (1)..(603)  
 US-09-899-429A-13  
 Alignment Scores: 4,420-94 Length: 603  
 Pred. No.: 941-00 Matches: 161  
 Score:

Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DE: 9 Gaps: 0  
 US-09-899-735-2 (1-161) X US-09-899-429A-13 (1-603)  
 QY 1 AspSerValCysProGlnGlyLysTyrIleHisPheGlnAsnAsnSerIleCysCysThr 20  
 DB 121 GATAGTGCTGCTCCCAAGGAAATATATATCCACCTCCAAATATTCGATTCCTGATCC 180  
 QY 21 LysCysHisLysGlyTyrTyrIleCysAsnAsnCysPheGlyPheGlyGlnSerThrAsp 40  
 DB 181 AAGTCCACAAAGAAACCTATATCTTAATGATCTGTCAGGCGCGCGGAGATATCGAC 240  
 QY 41 CysArgGluCysGlnSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu 60  
 DB 241 TCGAGGACATCTGAAAG 300  
 QY 61 SerCysSerLysCysArgLysGlnMetGlyGlnValHisIleSerSerCysThrValAsp 80  
 DB 301 AAGTCCACAAAGAAACCTATATCTTAATGATCTGTCAGGCGCGGAGATATCGAC 360  
 QY 81 ArgAspThrValCysGlyCysArgLysAsnGlnTyrArgHisTyrIlePheGlnAsnLeu 100  
 DB 361 CCGGAAATCTGAG 420  
 QY 101 PheGlnCysPheAsnGlySerLeuGlnGlyThrValHisLeuSerCysGlnGlu 120  
 DB 421 TCGAGGACATCTGAAAG 480  
 QY 121 LysGlnAsnThrValCysThrCysHisAlaGlyPhePheLeuArgGluAsnGluCysVal 140  
 DB 481 AAAAGAAACAGCGTGACCTGCATGCGAGGTTCTTTCTTAAGAGAAAAACAGGTGTC 540  
 QY 141 SerCysSerLysCysArgLysGlnMetGlyGlnValHisIleSerSerCysThrValAsp 160  
 DB 541 TCGAGGACATCTGAAAG 600  
 QY 161 Asn 161  
 DB 601 AAT 603  
 RESULT 13  
 US-09-899-429A-7  
 / Sequence 7, Application US/09899429A  
 / Patent No. US20020169118A1  
 / GENERAL INFORMATION:  
 / APPLICANT: Hauptmann, Rudolph  
 / APPLICANT: Hammler, Adolph  
 / APPLICANT: Maurer-Fogy, Ingrid  
 / APPLICANT: Stratowa, Christian  
 / TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for  
 / FILE REFERENCE: 98-385-J  
 / CURRENT APPLICATION NUMBER: US/09/899-429A  
 / CURRENT FILING DATE: 2001-07-03  
 / PRIOR APPLICATION NUMBER: 08/477,636  
 / PRIOR FILING DATE: 1995-06-07  
 / PRIOR APPLICATION NUMBER: 08/383,676  
 / PRIOR FILING DATE: 1995-02-01  
 / PRIOR APPLICATION NUMBER: 08/153,287  
 / PRIOR FILING DATE: 1993-11-17  
 / PRIOR APPLICATION NUMBER: 07/821,750  
 / PRIOR FILING DATE: 1992-01-02  
 / PRIOR APPLICATION NUMBER: 07/511,430  
 / PRIOR FILING DATE: 1990-04-20  
 / NUMBER OF SEQ ID NOS: 97  
 / SOFTWARE: PatentIn Ver. 2.0  
 / SEQ ID NO 7  
 / LENGTH: 603

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; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: recombinant
; OTHER INFORMATION: TNF-RP sequence
; NAME/KEY: CDS
; LOCATION: (1)..(633)
US-09-899-429A-7

Alignment Scores:
Pred. No.: 4,74e-94 Length: 633
Score: 941.00 Matches: 161
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DH: 9 Gaps: 0

US-09-882-735-2 (1-161) x US-09-899-429A-7 (1-633)
QY 1 AspSerValCysProGlnGlyLysTyrIleHisProGlnAnsnAnsrIleCysCysThr 20
DB 121 GATATGTCGTCTCTCCCAAGGAAATATATCCACCTCCAAATAATTCGATTTCGTGACC 180
QY 21 LysCysHisLysGlyThrTyrLeuTyrAsnAspCysProGlyProGlyGlnAspThrAsp 40
DB 181 AAGTCCCAACAAAGAACCTACTTCTACAAATGACTGTCCAGGCGCGGGGAGATACGAC 240
QY 41 CysArgGluCysGluSerGlySerPheThrAlaSerGluAnsnHisLeuArgHisCysLeu 60
DB 241 TCCAGGAGATCTACAGAGGAGTCTCTCCACCGCTTCAGAAACACCTCCAGACACTGCC 300
QY 61 SerCysSerLysCysArgGluMetGlyGlnValGluIleSerSerCysThrValAsp 80
DB 301 AATGTCCTCAATATCCAAATCCAAAGTAAATATGTCAGGTGAGATCTCTCTCCACAGT 360
QY 81 ArgAspThrValCysGlyCysArgLysAsnGlnTyrArgHisTyrTrpSerGluAnsnLeu 100
DB 361 CGGAAACAAACAGGTGTATATGTCAGGAGAACCCAGTACCGGCAATATTCGAGTGA 420
QY 101 PheGlnCysPheAsnCysSerLeuCysLeuAnsnGlyThrValHisLeuSerCysGlnGlu 120
DB 421 TTCTGATATTAATGAGCTTTGCTCAATGGACCGTGCACCTCTCTGCCAGGAG 480
QY 121 LysGlnAnsnThrValCysThrCysHisAlaGlyPhePheLeuArgGluAnsnGlyVal 140
DB 481 AAAACAAACAGGTGTATATGTCAGGAGAACCCAGTACCGGCAATATTCGAGTGA 540
QY 141 SerCysSerAsnCysLysLysSerLeuGluCysThrLysLeuCysLeuProGlnIleGlu 160
DB 541 TCTTGATATTAATGAGCTTTGCTCAATGGACCGTGCACCTCTCTGCCAGGAG 600

QY 161 Asn 161
DB 601 AAT 603

RESULT 14
US-09-756-186-7
; Sequence 7, Application US/09756186
; Patent No. US20010014333A1
; GENERAL INFORMATION:
; APPLICANT: Campbell, Robert K.
; APPLICANT: Jameson, Bradford A.
; APPLICANT: Chappel, Scott C.
; TITLE OF INVENTION: HYBRID PROTEINS
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street N.W., Ste 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 22207
; COMPUTER READABLE FORM:

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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/756,186
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/804,166
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Browdy, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: CAMPBELL=2A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
; INFORMATION FOR SEQ ID NO. 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1301 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 279..1287
US-09-756-186-7

Alignment Scores:
Pred. No.: 1.33e-93 Length: 1301
Score: 941.00 Matches: 161
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-09-882-735-2 (1-161) x US-09-756-186-7 (1-1301)
QY 1 AspSerValCysProGlnGlyLysTyrIleHisProGlnAnsnAnsrIleCysCysThr 20
DB 345 GATATGTCGTCTCTCCCAAGGAAATATATCCACCTCCAAATAATTCGATTTCGTGACC 404
QY 21 LysCysHisLysGlyThrTyrLeuTyrAsnAspCysProGlyProGlyGlnAspThrAsp 40
DB 405 AAGTCCCAACAAAGAACCTACTTCTACAAATATATGTCAGGTGAGATCTCTCTCCACAGT 464
QY 41 CysArgGluCysGluSerGlySerPheThrAlaSerGluAnsnHisLeuArgHisCysLeu 60
DB 465 TCCAGGAGATCTACAGAGGAGTCTCTCCACCGCTTCAGAAACACCTCCAGACACTGCC 624
QY 61 SerCysSerLysCysArgLysGluMetGlyGlnValGluIleSerSerCysThrValAsp 80
DB 525 AAGTCCCAACAAAGAACCTACTTCTACAAATATATGTCAGGTGAGATCTCTCTCCACAGT 584
QY 81 ArgAspThrValCysGlyCysArgLysAsnGlnTyrArgHisTyrTrpSerGluAnsnLeu 100
DB 585 CGGACACACCGGTGTATATGTCAGGAGAACCCAGTACCGGCAATATTCGAGTGA 644
QY 101 PheGlnCysPheAsnCysSerLeuCysLeuAnsnGlyThrValHisLeuSerCysGlnGlu 120
DB 645 TTCAGGTGCTTCAATTCAGGCGCTCTCTCTCAATGGACCGTGCACCTCTCTGCCAGGAG 704
QY 121 LysGlnAnsnThrValCysThrCysHisAlaGlyPhePheLeuArgGluAnsnGlyVal 140
DB 705 AAACAGAACACCGGTGTATATGTCAGGAGAACCCAGTACCGGCAATATTCGAGTGA 764
QY 141 SerCysSerAsnCysLysLysSerLeuGluCysThrLysLeuCysLeuProGlnIleGlu 160
DB 765 TCTTGATATTAATGAGCTTTGCTCAATGGACCGTGCACCTCTCTGCCAGGAG 824

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CY 161 Asn 161  
DB 825 AAT 827

## RESULT 15

US-09-898-234-11  
Sequence 11, Application US/09898234  
Patent No. US2002015112A1  
GENERAL INFORMATION  
APPLICANT: Hauptmann, Rudolph  
APPLICANT: Hummeler, Adolph  
APPLICANT: Maurer-Peggy, Ingrid  
APPLICANT: Strietowa, Christian  
TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for  
FILE REFERENCE: 98,385-1  
CURRENT APPLICATION NUMBER: US/09/898,234  
CURRENT FILING DATE: 2001-07-03  
PRIORITY APPLICATION NUMBER: 98/525,998  
PRIORITY FILING DATE: 2000-03-15  
PRIORITY APPLICATION NUMBER: 98/383,676  
PRIORITY FILING DATE: 1995-02-01  
PRIORITY APPLICATION NUMBER: 08/153,287  
PRIORITY FILING DATE: 1993-11-17  
PRIORITY APPLICATION NUMBER: 07/622,750  
PRIORITY FILING DATE: 1992-01-02  
PRIORITY APPLICATION NUMBER: 07/511,430  
PRIORITY FILING DATE: 1990-04-20  
NUMBER OF SEQ ID NOS: 87  
SOFTWARE: Patent Ver. 2.0  
SEQ ID NO 11  
LENGTH: 1334  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1231..(1325)  
OTHER INFORMATION: Description of Artificial Sequence: cDNA insert of  
OTHER INFORMATION: Lambda-TNF E15 and pTNF-BP15 vectors  
US-09-898-234-11

## Alignment Scores:

Pred. No.:	1,38e-93	Length:	1334
Score:	941.00	Matches:	161
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	9	Gaps:	0

US-09-882-735-2 (1-161) X US-09-898-234-11 (1-1334)

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CY 1 AAPSCTVNAICYSPTGGINQIYLYETTYTILHISPROGIIASRAENSRILEQSCYSTHR 20
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CY 21 LYSCTHLESLYSGLITHTYILEUTYLASNAAPCYSPROGIYPROGIYGLINASPTHRASP 40
DB 387 AAGTGTGCTAAAGGAACTACTGTGATATATATGTCTCAAGTCCCGGCGAGATACGAGC 452
CY 41 CYSATGSLVUCYSGIUSGICYSERGLYSERPHETHTALASERGIIASRHSISLEUARGHS 60
DB 453 TCGATGATGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 512
CY 61 SERCYSSERLYSCYSAIGLYSGIUSGIIUSGIIUSGIIUSGIIUSGIIUSGIIUSGIIUS 80
DB 518 AAGTGTGCTAAAGGAAATATATVCCACCTCCAAAATATATGATTTGCTGTACC 572
CY 81 ATGATTTTVALCYSGII CYSAIGLYSASNSITLYARGHSITLYITPSERGIIUSNLEU 100
DB 573 CGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 632
CY 121 PHEGICNYTPEASRCYSSERLYCYSLEASNGIYTHRTVALHISLEUSERCYSGINGIU 120

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DB 633 ITCCAGTCTTCCAAATVCGAGCCTCTGACCTCAATGGAGCCGTCACCTCTCCCGAGAG 692
CY 121 LYSGLINASNTHTVALCYSTHRCYSHISALAGLYPHEPHELEUARGGLIUSNGIUCYSVAL 140
DB 693 AAACGAGAACCGGTGTGACCTGCGCATGCAAGTTCTTTCTTAAGAGAAAAAGAGTGTCTC 752
CY 141 SERCYSSERLYSCYSLVYSERLEUGIUCYTHRTYLSLEUCYSLLEUPROGINILEGIU 160
DB 753 TCGATGATGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 812
CY 161 Asn 161
DB 813 AAT 815

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Search completed: January 6, 2003, 04:13:57  
Job time : 281 secs



GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

CM protein - nucleic search, using frame\_plus\_p2n model

Run on: January 6, 2003, 04:09:21, Search time 2190 Seconds  
(without alignments)  
1190.627 Million cell updates/sec

Title: US-09-882-735-2

Perfect score: 941

Sequence: 1 DSVCPQGYTHPQNNSICT .....CSNCFKSLCTKLCPLQIEN 161

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Xgapop 10.0, Xgapext 0.5  
Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 16154066 seqs, 8097743176 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-DH-EST\_OPMT=fastap -SUFFIX=ist -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
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DOCALIGN=200 -THP\_SCORE=pt -THP\_MAX=100 -THP\_MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=pt -NORM=ext -HAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-UOFF=US09882735.acfn.1.1.763.runat\_03012003\_074146\_17227 -ICPU=3  
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-YCAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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2: em\_esthum:  
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8: em\_hic:  
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10: qb\_est2:  
11: qb\_hic:  
12: qb\_est3:  
13: qb\_est4:  
14: qb\_est5:  
15: em\_estfun:  
16: em\_estom:  
17: qb\_gss:  
18: em\_gss\_hum:  
19: em\_gss\_inv:  
20: em\_gss\_pln:  
21: em\_gss\_vit:  
22: em\_gss\_fun:  
23: em\_gss\_mam:  
24: em\_gss\_mus:  
25: em\_gss\_other:  
26: em\_gss\_pro:  
27: em\_gss\_rod:

Prd. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
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4	937	99.6	761	9	AU111978	AU111978 AU131978
5	932	99.0	837	9	AL522989	AL522989 AL522989
6	931	98.9	1070	13	BMS46826	BMS46826 AGENTCORT
7	917	97.4	994	14	BMS00044	BMS00044 AGENTCORT
8	908	96.5	918	13	RI821169	RI821169 601015648
9	903	96.0	975	9	AL577008	AL577008 AL577008
10	892	94.8	859	13	BI870917	BI870917 603404442
11	888	94.4	942	9	AL529836	AL529836 AL529836
12	879	93.4	969	12	BE871809	BE871809 601448388
13	868	92.2	872	13	BI769006	BI769006 603018164
14	864	91.8	845	9	AU125021	AU125021 AU125021
15	859.5	91.3	916	13	BI757305	BI757305 604029419
16	848	90.1	859	9	AU124446	AU124446 AU124446
17	846	89.9	767	9	AU142156	AU142156 AU142156
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20	817	86.8	772	9	AU137990	AU137990 AU137990
21	816.5	86.8	971	12	BE876920	BE876920 601488440
22	815.5	86.7	823	13	BI766980	BI766980 603054805
23	815	86.6	936	12	BG681438	BG681438 602528106
24	793	84.3	951	14	BQ882704	BQ882704 AGENTCORT
25	792	84.2	475	12	BE710028	BE710028 AL3 HT041
26	790.5	84.0	929	12	BQ677121	BQ677121 602623792
27	785	83.4	817	9	AU125680	AU125680 AU125680
28	781	83.0	913	14	BQ26409	BQ26409 AGENTCORT
29	771	81.9	712	10	BE549214	BE549214 601078765
30	763	81.1	846	13	BI917624	BI917624 603183744
31	757	80.4	706	9	AU124156	AU124156 AU124156
32	737	78.3	934	13	RI831497	RI831497 603074413
33	728	77.4	387	14	BQ335492	BQ335492 JMA MT043
34	727	77.3	834	9	AU126303	AU126303 AU126303
35	718	76.3	415	12	BG001080	BG001080 CV1 GN020
36	713	75.8	822	13	BI269829	BI269829 602471043
37	711	75.6	491	12	BF839822	BF839822 K3 H1023
38	708	75.2	826	13	BI772771	BI772771 603059449
39	696	74.0	788	9	AU124519	AU124519 AU124519
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41	691.5	73.5	805	9	AU125694	AU125694 AU125694
42	684	72.7	761	12	BG382718	BG382718 602406578
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# ALIGNMENTS

RESULT 1  
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LOCUS B0723672 931 bp mRNA linear EST 16 JUL 2002  
DEFINITION AGENTCORT\_8489850 lupski\_dorsal\_root\_ganglion Homo sapiens cDNA  
clone IMAGE:6184295 5', mRNA sequence.  
ACCESSION B0723672  
VERSION B0723672.1 GI:218622569  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 931)  
AUTHORS NIH-MGC <http://mgc.ncbi.nih.gov/>  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL COMMENT  
 Unpublished (1999)  
 Contact: Robert Strausberg, Ph.D.  
 Email: c9apbs-remail.nih.gov  
 Tissue Procurement: Dr. James R. Lupski  
 cDNA Library Preparation: Life Technologies, Inc.  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: L1AM13573 row: d column: 24  
 High quality sequence stop: 607.

## FEATURES

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Location/Qualifiers  
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 /clone\_lib="Lupski\_dorsal\_root\_ganglion"  
 /sex="male"  
 /tissue\_type="dorsal root ganglia"  
 /dev\_stage="adult, 36 yr"  
 /lab\_host="DH10B"  
 /note="Vector: PCMV-SPORT6 (Life Technologies); Site 1:  
 NotI; Site 2: SalI; cDNA made by oligo-dT priming.  
 Directionally cloned using the following adaptors:  
 5'-TCGACCCACGAGTCCG-3' and  
 5'-GACTAGTCTAGATCGGAGCGGCGCTT(15)-3'. Size selected >  
 1 kb for average insert length 1.7 kb. This is a primary  
 library, non-amplified. Library constructed by Life  
 Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor  
 College of Medicine) and is available through Life  
 Technologies."

BASE COUNT 213 a 283 c 224 g 204 t 2 others  
 ORIGIN

## Alignment Scores:

Pred. No.: 2,35e-92 Length: 931  
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 Percent Similarity: 100.00% Conserved: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 14 Gaps: 0

US-09-882-735-2 (1-161) x BQ723672 (1-931)

QY 1 AspSerValCysProGlnGlyLysTyrIleHisProGlnAsnSerIleCysCysThr 20  
 Db 11 GATAGTGTGTGTCCTCCCAAGAAATATATCCACCTCAAAATATGATTCCTGTAC 70  
 QY 21 LysCysHisLysGlyThrTyrLeuTyrAsnAspCysProGlyProGlyGlnAspThr 40  
 Db 71 AAGTGTCCCAAAAGAACCTACTGTGACATGACTGTCCAGGCCGGGAGGATACGGAC 130  
 QY 41 CysArgGlnCysGlnSerGlySerPheThrAlaSerGlnAsnHisLeuArgHisCysLeu 60  
 Db 111 TGCAGGAGAGTGTGAAGGAGGCTCTCCCTCAGACCAACCACTCAGACACTGCTC 190  
 QY 61 SerCysSerLysCysArgLysGlnMetGlyGlnValGlnIleSerSerCysThrValAsp 80  
 Db 151 AATGTGTGCAATGTCCCAAGAAATATATCCACCTCAAAATATGATTCCTGTAC 250  
 QY 81 ArgAspThrValCysGlyCysArgLysAsnGlnTyrArgHisTyrTyrSerGlnAsnLeu 100  
 Db 251 CCGAGACCTGT 310  
 QY 101 PheGlnCysPheAsnCysSerLeuCysLeuAsnGlyThrValHisLeuSerCysGlnGln 120  
 Db 311 TGCAGGAGAGTGTGAAGGAGGCTCTCCCTCAGACCAACCACTCAGACACTGCTC 370  
 QY 121 LysThrAspThrValCysThrCysHisAlaGlyPhePheLeuArgGlnAsnGlnCysVal 140  
 Db 371 AAAAGAGACCTGT 430

QY 141 SerCysSerAsnCysLysLysSerLeuGlnCysThrLysLeuCysLeuProGlnIleGln 160  
 Db 431 TCTGTGTAGTACTGTAGAAAAGCTGAGATGTCACCAAGATTGTGCTTACCCAGATTGAG 490  
 QY 161 Asn 161  
 Db 491 AAT 493

## RESULT 2

AL559050

LOCUS

DEFINITION

AL559050 LTR\_NFL008\_TG2 Homo sapiens cDNA clone CS0DD010YB05 5

prime, mRNA sequence.

ACCESSION

AL559050

VERSION

AL559050.1 GI:12904166

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

1. (bases 1 to 957)

AUTHORS

Li, W.B., Gruber, C., Jesse, J. and Polayes, D.

TITLE

Full-length cDNA libraries and normalization

JOURNAL

Unpublished (2001)

COMMENT

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: segref@genoscope.cns.fr, Web: www.genoscope.cns.fr.

Location/Qualifiers

1..957

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="CS0DD010YB05"

/clone\_lib="LTR\_NFL008\_TG2"

/sex="male"

/tissue\_type="T cells from T cell leukemia"

/note="Vector: PCMVSPORT 6; Site 1: NotI; 1st strand cDNA

was primed with a NotI-oligo(dT) primer. Five prime end

enriched, double-stranded cDNA was digested with Not I and

cloned into the Not I and Eco RV sites of the PCMVSPORT 6

vector. Library was normalized. Library was constructed by

Life Technologies. Contact: Feng Liang Life Technologies,

a division of Invitrogen 9800 Medical Center Drive

Rockville, Maryland 20850, USA Fax: (1) 301 610 8371

Email: fliang@lifetech.com URL:

http://fulllength.invitrogen.com"

BASE COUNT 222 a 262 c 252 g 220 t 1 others

ORIGIN

## Alignment Scores:

Pred. No.: 2,45e-92 Length: 957  
 Score: 941.00 Matches: 161  
 Percent Similarity: 100.00% Conserved: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 9 Gaps: 0

US-09-882-735-2 (1-161) x AL559050 (1-957)

QY 1 AspSerValCysProGlnGlyLysTyrIleHisProGlnAsnSerIleCysCysThr 20  
 Db 313 GATAGTGTGTGTCCTCCCAAGAAATATATCCACCTCAAAATATGATTCCTGTAC 372  
 QY 21 LysCysHisLysGlyThrTyrLeuTyrAsnAspCysProGlyProGlyGlnAspThr 40  
 Db 373 AAGTGTCCCAAAAGAACCTACTGTGACATGACTGTCCAGGCCGGGAGGATACGGAC 432  
 QY 41 CysArgGlnCysGlnSerGlySerPheThrAlaSerGlnAsnHisLeuArgHisCysLeu 60  
 Db 433 TGCAGGAGAGTGTGAAGGAGGCTCTCCCTCAGACCAACCACTCAGACACTGCTC 492  
 QY 61 SerCysSerLysCysArgLysGlnMetGlyGlnValGlnIleSerSerCysThrValAsp 80

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Db 493 AACTGCTGCAAAATGCTTCAAGTTCAGATCTTTTTCACAGTGGAC 552
Oy 81 ArgAspThrValCysGlyCysArgLysAsnGlnTyrArgHisTyrTTPSerGluAsnLeu 100
Db 553 CAGGATATGCTGTTGATGATGAGAAAGAGTACAGGATATTATTGAGTGAAGACCTT 612
Oy 101 PheGlnCysPheAsnCysSerLysCysLeuAsnGlyThrValHisLeuSerCysGlnGlu 120
Db 613 TTCCAGTGTCTTCAATTCAGATCTTTCCTTAATGAGAGTCTGACCTCTCTCCGCAAGAG 672
Oy 121 LysGlnAsnThrValCysThrCysHisAlaGlyPhePheLeuArgGluAsnGluCysVal 140
Db 673 AAAACAAACATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCT 732
Oy 141 SerCysSerAsnCysLysLysSerLeuGluCysThrLysLeuCysLeuProGlnIleGlu 160
Db 733 TCTGTAGTAACTGTAACAAAAGGCTGATGATGATGATGATGATGATGATGATGATGATG 792
Oy 161 Asn 161
Db 793 AAT 795

RESULT 3
LOCUS RG180101 974 bp mRNA linear EST 06-FEB-2001
DEFINITION 602129676P1 NIH_MGC_91 Homo sapiens cDNA clone IMAGE:4431019 5',
mRNA sequence.
ACCESSION RG180101
VERSION RG180101.1 GI:125484804
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 974)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/DTF
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L14M10185, row: g, column: 20
High quality sequence stop 657
FEATURES
Location/Qualifiers
source 1..974
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4431019"
/tissue_type="adnocarcinoma, cell line"
/lab_hosts="DH10B (phage-resistant)"
/note="Organ: prostate; Vector: pCMV-SPORT6; Site 1: Not I;
Site 2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.4 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC library."
BASE COUNT 259 a 265 c 265 g 185 t
ORIGIN
Alignment Scores:
Pred. No.: 2,53e-92 Length: 974
Score: 941.00 Matches: 161
Percent Similarity: 100.00% Conservative: 0
Best local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
PR: 12 Gaps: 0

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us-09-882-735-2 (1 161) x RG180101 (1 974)
Oy 1 AspSerValCysProGlnGlyLysTyrIleHisProGlnAsnAsnSerIleCysCysThr 20
Db 118 GATAGTGTGTCTCCCAAGGAGAAATATATGCAAGCTTAAAAATAATTGATTTAACTATG 177
Oy 21 LysCysHisLysGlyThrTyrLeuTyrAsnAspCysArgGlyPheGlyGlnAspThrAsp 40
Db 178 AAGTGCACACAAAAGAACTTACTTGTATATGATCTTAAAGAGGAGGAGGAGGAGGAGGAG 247
Oy 41 CysArgGluCysGluSerGlySerPheThrAlaSerGlnAsnHisLeuArgHisLysLeu 60
Db 238 TGCAGGAGAGTGTGAGAGAGCTGCTCTTAAAGGCTTCAAAAACCACTTCAAGATTAAG 297
Oy 61 SerCysSerLysCysAspGlyGluMetGlyGlnValGluIleSerSerCysThrValAsp 80
Db 298 AATGCTCTCAAAATGCTCAAAAAGGAGAAATGAGTCAAGTCAATATATTAAGTAAAT 447
Oy 81 ArgAspThrValCysGlyCysArgLysAsnGlnTyrArgHisTyrTTPSerGluAsnLeu 100
Db 358 CCGGACACCCGTGTGTGCTGCAGGAGAACCACTATATTAAGTAAATTAAGTAAATTAAG 417
Oy 101 PheGlnCysPheAsnCysSerLeuCysLeuAsnGlyThrValHisLeuSerCysGlnIle 120
Db 418 TTCAGTGTCTTCAATTCAGAGCTCTGCTTCAAGGAGAGAGTCAAGTCTTCAAGGAGAG 477
Oy 121 LysGlnAsnThrValCysThrCysHisAlaGlyPhePheLeuArgGluAsnGluCysVal 140
Db 478 AAAACAGAACACCGTGTGCTGACCTGCAATGAGATTTTCTTAAAGAGAGAGAGAGAG 537
Oy 141 SerCysSerAsnCysLysLysSerLeuGluCysThrLysLeuCysLeuProGlnIleGlu 160
Db 538 TCTGTAGTAACTGTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 597
Oy 161 Asn 161
Db 598 AAT 600

RESULT 4
LOCUS AU131978 761 bp mRNA linear EST 01-APR-2002
DEFINITION AU131978 NT2RP3 Homo sapiens cDNA clone NT2RP3003570 5', mRNA
sequence.
ACCESSION AU131978
VERSION AU131978.1 GI:10992332
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 761)
AUTHORS Ota, T., Nishikawa, T., Suzuki, Y., Ishii, S., Saito, K., Kawai, Y.,
Yamamoto, J., Wakamatsu, A., Nakamura, Y., Nagai, T., Sugano, S., and
Isogai, T.
TITLE HRI human cDNA project
JOURNAL Unpublished (2000)
COMMENT Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisakazu, Chiba 292 0812, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: genomics@hri.co.jp
BASE COUNT 259 a 265 c 265 g 185 t
ORIGIN
Alignment Scores:
Pred. No.: 2,53e-92 Length: 761
Score: 941.00 Matches: 161
Percent Similarity: 100.00% Conservative: 0
Best local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
PR: 12 Gaps: 0
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Location/Qualifiers
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/db_xref="taxon:9606"
/clone="NT2RP3003570"

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/cell\_type="teratocarcinoma"  
/cell\_line="NT2"  
/note="Vector: PMEL8FL3; mRNA from NT2 neuronal precursor  
cells after 2-weeks retinoic acid (RA) induction"  
BASE COUNT 178 a 199 c 201 g 179 t 4 others  
ORIGIN

## Alignment Scores:

Pred. No.	4,61e-32	Length:	761
Score:	937.00	Matches:	160
Percent Similarity:	99.38%	Conservative:	0
Best Local Similarity:	99.38%	Mismatches:	1
Query Match:	99.57%	Indels:	0
DB:	9	Gaps:	0

US-09-882-735-2 (1-161) x A0131978 (1-761)

QY 1 AspSerValCysProGlnGlyLysThrTleHisProGlnAsnSerIleCysCysThr 20  
DB 182 GATAGTGTGTGTCCTCCAGGAAATATATCCACTTCAAAATATTCGATTCTGTACC 241  
QY 21 LysCysHisLysGlyThrTyrLeuTyrAsnAspCysProGlyProGlyGlnAspThrAsp 40  
DB 242 AAGTCCCAAGAGAACTACTGTACATGACGTCCAGGCCCGGGGAGATACGGAC 301  
QY 41 CysArgGluCysGluSerGlySerThrThrAlaSerGluAsnHisLeuArgHisCysLeu 60  
DB 302 TCCAGGAGATGTGAGAGGGGCTCCCTTCACCCCTTCAGAAAACCACTCAGACAGTGCCTC 361  
QY 61 SerCysSerLysCysArgLysGluLysGlnValGlnLeuSerSerCysThrValAsp 80  
DB 362 AGTTATTTAAATATCCAAABAAATATATATATATATATATATATATATATATATATAT 421  
QY 81 ArgAspThrValCysGlyCysArgLysAsnGlnTyrArgHisTyrTyrSerGluAsnLeu 100  
DB 422 CCGGACACCGGCTGT 481  
QY 121 PheGlnCysPheAsnCysSerLeuCysLeuAsnGlyThrValHisLeuSerCysGlnGlu 120  
DB 482 TTCCAGTGTCTTCAAT 541  
QY 141 LysGlnAsnThrValCysThrCysHisAlaGlyPhePheLeuArgGluAsnGluCysVal 140  
DB 542 AAACGAGAACCGGT 601  
QY 161 SerCysSerAsnGlyLysLysSerLeuGluCysThrTyrLeuCysLeuProGlnIleGlu 160  
DB 602 TNCCTATATTAATCTGTAAAGAAAACCTGTATGTACAGAAATGTGTGTGTGTGTGTGTGT 661  
QY 161 Asn 161  
DB 662 AAT 664

RESULT 5  
LOCUS AL522989 837 bp mRNA linear EST 13-FEB-2001  
DEFINITION AL522989.1:111-111:04:3802 Homo sapiens cDNA clone CGDB009YPI4 5  
ACCESSION AL522989  
VERSION AL522989.1 GI:12786452  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 837)  
AUTHORS Li, W. B., Gruber, C., Jessee, J., and Polayes, D.  
TITLE Full-length cDNA libraries and normalization  
JOURNAL Unpublished (2001)  
CONTACT: Genoscope  
Genoscope - Centre National de Sequencage  
BP 191 91006 Evry cedex - France  
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr.

FEATURES  
source

Location/Qualifiers  
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/db\_xref="taxon:9606"  
/clone="CSDB009YPI4"  
/clone\_1ib="LTI\_NFL004\_NBC2"  
/sex="male"  
/tissue\_type="neuroblastoma cells"  
/lab\_host="DH10B"  
/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA  
was primed with a NotI-oligo(dT) primer. Five prime end  
enriched, double-stranded cDNA was digested with NotI and  
cloned into the NotI and EcoRV sites of the pCMVSPORT 6  
vector. Library was normalized. Library was constructed  
by Life Technologies. Contact: Feng Liang Life  
Technologies, a division of Invitrogen 9800 Medical Center  
Drive Rockville, Maryland 20850, USA Fax: (1) 301 610  
8371 Email: fliang@lifetech.com URL:  
http://fulllength.invitrogen.com"

BASE COUNT 199 a 231 c 229 g 177 t 1 others  
ORIGIN

## Alignment Scores:

Pred. No.	1.9e-91	Length:	837
Score:	932.00 <td>Matches:</td> <td>160 </td>	Matches:	160
Percent Similarity:	99.38% <td>Conservative:</td> <td>0 </td>	Conservative:	0
Best Local Similarity:	99.38% <td>Mismatches:</td> <td>1 </td>	Mismatches:	1
Query Match:	99.04% <td>Indels:</td> <td>0 </td>	Indels:	0
DB:	9 <td>Gaps:</td> <td>0 </td>	Gaps:	0

US-09-882 735-2 (1-161) x AL522989 (1-837)

QY 1 AspSerValCysProGlnGlyLysThrTleHisProGlnAsnSerIleCysCysThr 20  
DB 318 GATAGTGTGTGTCCTCCAGGAAATATATCCACCCCAAAATATTCGATTGTGTGTACC 377  
QY 21 LysCysHisLysGlyThrTyrLeuTyrAsnAspCysProGlyProGlyGlnAspThrAsp 40  
DB 378 AAGTCCCAAGAGAACTACTGTACATGACGTCCAGGCCCGGGGAGATACGGAC 437  
QY 41 CysArgGluCysGluSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu 60  
DB 438 TGCAGGAGGTGTGAGAGCGGCTCTTCACCGCTTCAGAAAACCACTCAGACAGCTC 497  
QY 61 SerCysSerLysCysArgLysGluLysGlnValGlnLeuSerSerCysThrValAsp 80  
DB 498 AGCTGCTCCAAATGCCGAAAGAAATGGGTGAGATGTCTTCTTGTGACAGTGGAC 557  
QY 81 ArgAspThrValCysGlyCysArgLysAsnGlnTyrArgHisTyrTyrSerGluAsnLeu 100  
DB 558 CGGACACCGT 617  
QY 101 PheGlnCysPheAsnCysSerLeuCysLeuAsnGlyThrValHisLeuSerCysGlnGlu 120  
DB 618 TTCAGTGTCTTCAATATGACAGCTCTGCTCAATATGGAGACCGTGCACCTCTCTGCAGAG 677  
QY 121 LysGlnAsnThrValCysThrCysHisAlaGlyPhePheLeuArgGluAsnGluCysVal 140  
DB 678 AAACGAGAACCGGT 737  
QY 141 SerCysSerAsnGlyLysLysSerLeuGluCysThrTyrLeuCysLeuProGlnIleGlu 160  
DB 738 TCCGTGTATTAATCTGTAAAGAAAACCTGTATGTACAGAAATGTGTGTGTGTGTGTGTGT 797  
QY 161 Asn 161  
DB 798 AAT 800

RESULT 6  
LOCUS BM546826 1070 bp mRNA linear EST 20-FEB-2002  
DEFINITION BM546826:6491128 NIH\_MGC\_125 Homo sapiens cDNA clone IMAGE:5723557  
5', mRNA sequence.



BASE DATA  
ORIGIN

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0DI082YA01"
/clone_1b="LTI NPL006 PL2"
/tissue_type="placenta"
/notes="Vector: pCMVSPORT 6; Site 1: NotI; 1st strand
enriched, double-stranded cDNA was digested with NotI
cloned into the Not I and Eco RV sites of the pCMVSP

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[illegible]

QY	160	UASN	161
Db	833	GAAT	836
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RESULT 12			
LOCUS	BES71809	969 bp	mRNA linear EST 20-OCT-2000
DEFINITION	c01d4b3bfef1 NIH_MGC_c5 Homo sapiens cDNA clone IMAGE:385255 5'.._		
ACCESSION	BES71809		
VERSION	BES71809.1	GI:10320585	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Ekarjota, Metazoa; Chordata, Craniata, Vertebrata, Euteleostomi;		
AUTHORS	Mammalia, Eutheria; Primates, Catarrhini; Hominidae, Homo.		
TITLE	1 (bases 1 to 969)		
JOURNAL	NIH-MGC http://mgc.nci.nih.gov/.		
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)		
	Contact: Robert Strausberg, Ph.D. Email: cgabbs-r@mail.nih.gov Tissue Procurement: ATCC CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <a href="http://image.llnl.gov">http://image.llnl.gov</a> Plate: LHAM9574 row: o column: 22 High quality sequence stop: 642.		
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	/db_xref="taxon:9606"		
	/clone="IMAGE:385255"		
	/clone_1lb="NIH_MGC_65"		
	/tissue_type="adenocarcinoma"		
	/lab_host="VDH10B (phage-resistant)"		
	/note="Organ: colon; Vector: pCMV-SPORT6, Site: 1..Notif; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size: 1.8 kb. Library constructed by Life Technologies."		
EASE COUNT	281 a	273 c	241 g 174 t
ORIGIN			
<hr/>			
Alignment Scores:			
Pred. No.:	1,52e+85	Length:	969
Score:	879.00	Matches:	153
Percent Similarity:	98.71%	Conservative:	0
Best Local Similarity:	98.71%	Mismatches:	1
Query Match:	93.41%	Indels:	1
DB:	12	Gaps:	0
<hr/>			
US-09-882-735-2 (1-161) X BES71809 (1-969)			
QY	8	Lysfyrtrllehis	-proglinasanserillecyseethlyscyehisylsglythyrtty 27
Db	2	AAATAATTCGGCGCCTCAAAAATAATTGATTTGGTGTAACAAGGCCAACAAACCTA	61
CY	27	rleutyasnaspocyprrogliproglglinaspthrAspcysArgqlucysgluberel	47
Db	62	CTTGTAACATGACTGTGCUAGGCCCGGAGAGATAAGACACACAGGTCAGACCGG	121
CY	47	yserpheThAlaseGlAsnhIsleuArHisicyleuseScySerlyscyArgly	67
Db	122	CTCCCTTACCCTTAGAAAAACACACTGACACTGTGCTCATGCTGCTCCAAAATGCCGAAA	181







GenCore version 5.1.3  
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GM nucleic - nucleic search, using sw model

Run on: January 6, 2003, 01:14:03 ; Search time 2774 Seconds  
(without alignments)  
5067 287 Million cell updates/sec

Title: US-09-882-735-1  
Perfect score: 483  
Sequence: 1 gataatgtgtgtcccaagg ... gactaccacagattgagaat 483

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 2054640 seqs, 1455140287A residues  
Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: GenEmbl.\*

- 1: gb.ba.\*
- 2: gb.htg.\*
- 3: gb.in.\*
- 4: gb.om.\*
- 5: gb.ov.\*
- 6: gb.pat.\*
- 7: gb.ph.\*
- 8: gb.pl.\*
- 9: gb.pr.\*
- 10: gb.ro.\*
- 11: gb.sts.\*
- 12: gb.sy.\*
- 13: gb.un.\*
- 14: gb.vi.\*
- 15: em.ba.\*
- 16: em.fun.\*
- 17: em.hum.\*
- 18: em.in.\*
- 19: em.mu.\*
- 20: em.om.\*
- 21: em.or.\*
- 22: em.ov.\*
- 23: em.pat.\*
- 24: em.ph.\*
- 25: em.pl.\*
- 26: em.ro.\*
- 27: em.sts.\*
- 28: em.un.\*
- 29: em.vi.\*
- 30: em.htg.hum.\*
- 31: em.htg.inv.\*
- 32: em.htg.other.\*
- 33: em.htg.mus.\*
- 34: em.htg.pln.\*
- 35: em.htg.rod.\*
- 36: em.htg.mam.\*
- 37: em.htg.vrt.\*
- 38: em.sy.\*
- 39: em.htgo.hum.\*
- 40: em.htgo.mus.\*
- 41: em.htgo.other.\*

Prod. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	483	100.0	483	6	A29099	A29099 Synthet ic n
2	483	100.0	483	6	AP174442	AP174442 Sequence
3	483	100.0	1301	6	AR111310	AR111310 Sequence
4	483	100.0	1301	6	AR134762	AR134762 Sequence
5	483	100.0	1331	6	A29103	A29103 H.sapiens
6	483	100.0	1368	6	A29098	A29098 Synthet ic n
7	483	100.0	2050	9	HUMINPRP	M60275 Human tumor
8	483	100.0	2062	6	A21522	A21522 TNF alpha
9	483	100.0	2062	6	I43805	I43805 Sequence
10	483	100.0	2067	9	HUMTNER	M43294 Human tumor
11	483	100.0	2159	9	AK956611	AK956611 Homo sapi
12	483	100.0	2111	6	A26412	A26412 cDNA for
13	483	100.0	2111	6	AX409713	AX409713 Sequence
14	483	100.0	2111	9	HUMTNERB	M59286 Homo sapiens
15	483	100.0	2112	9	HUMTNERC	M64121 Human tumor
16	483	100.0	2161	6	AP096330	AP096330 Sequence
17	483	100.0	2161	9	HSTNFR1A	X55113 H.sapiens
18	483	100.0	2175	6	A43873	A43873 Sequence
19	483	100.0	2175	6	A78738	A78738 Sequence
20	483	100.0	2175	6	AR041076	AR041076 Sequence
21	483	100.0	2175	6	I64751	I64751 Sequence
22	483	100.0	2176	6	AI9907	AI9907 Synthet ic n
23	483	100.0	2194	9	BC010140	BC010140 Homo sapi
24	483	100.0	6889	6	I26928	I26928 Sequence
25	483	100.0	6896	6	AR031375	AR031375 Sequence
26	483	100.0	6896	6	BD009743	BD009743 Composi
27	478.4	99.0	600	6	A20257	A20257 Synthet ic n
28	477	98.8	510	6	A21525	A21525 ol sequence
29	475.2	98.4	600	6	I43808	I43808 Sequence
30	475	98.3	1147	6	AR131309	AR131309 Sequence
31	475	98.3	1147	6	AR134761	AR134761 Sequence
32	471	97.5	2061	6	A20255	A20255 cDNA
33	424.4	87.9	1049	6	AR131307	AR131307 Sequence
34	424.4	87.9	1049	6	AR134759	AR134759 Sequence
35	424.4	87.9	1202	6	AR131308	AR131308 Sequence
36	424.4	87.9	1202	6	AR134760	AR134760 Sequence
37	383	79.3	504	6	A20713	A20713 Synthet ic n
38	383	79.3	504	6	I43813	I43813 Sequence
39	381	78.9	501	6	I43786	I43786 Sequence
40	379.8	78.6	1977	6	AX404869	AX404869 Sequence
41	372	77.0	372	6	A20253	A20253 Synthet ic n
42	372	77.0	372	6	I43787	I43787 Sequence
43	369	76.4	500	6	A20254	A20254 Synthet ic n
44	358.2	74.2	2171	4	AB051103	AB051103 Peptid
45	357.2	74.0	474	6	A20259	A20259 Synthet ic n

ALIGNMENTS

RESULT 1  
A29099  
LOCUS A29099 483 bp DNA linear PAT 03 JUL 1995  
DEFINITION Synthetic DNA for TNF-binding polypeptide from patient FRO100408.  
ACCESSION A29099  
VERSION A29099.1 GI:1248893  
KEYWORDS  
SOURCE synthetic construct.  
ORGANISM synthetic construct.  
REFERENCE 1 (bases 1 to 483)  
AUTHORS Hauptmann,R., Himmler,A., Maurer-Foyy,I. and Stratowa,R.  
TITLE TNF-receptor, TNF-binding protein and DNA coding therefor  
JOURNAL Patent: Ep 019438 A 49 24-OCT-1990;  
BOEHRINGER INGELHEIM INTERNATIONAL G.M.B.H

FEATURES  
 source  
 Location/Qualifiers  
 1..483  
 /organism="synthetic construct"  
 /db\_xref="taxon:32630"

BASE COUNT 130 a 124 c 123 g 106 t  
 ORIGIN  
 Query Match 100.0%; Score 483; DB 6; Length 483;  
 Best Local Similarity 100.0%; Pred. No. 5, 2e-141;  
 Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

27 1 GATAGTGTGTGTCCTCCCAAGGAAAAATATATACACCTCCAAATATATGATTGCTGTACC 60  
 Db 1 GATAGTGTGTGTCCTCCCAAGGAAAAATATATACACCTCCAAATATATGATTGCTGTACC 60  
 QY 61 AAGTGTCCCAAAAGGAACTTATTGTACATGATGTGTCAGGCGCGGAGGATACGGAC 120  
 Db 61 AAGTGTCCCAAAAGGAACTTATTGTACATGATGTGTCAGGCGCGGAGGATACGGAC 120  
 QY 121 TGCAGGAGGTGTGAGACCGGCTCTTACACCGCTTCAGAAAAACCACTCGACACTGCCCTC 180  
 Db 121 TGCAGGAGGTGTGAGACCGGCTCTTACACCGCTTCAGAAAAACCACTCGACACTGCCCTC 180  
 QY 181 AGCTGTCCAAATCCGAAAGAAATGGTCCAGTGAATCTCTTTGCAACAGTGGAC 240  
 Db 181 AGCTGTCCAAATCCGAAAGAAATGGTCCAGTGAATCTCTTTGCAACAGTGGAC 240  
 QY 241 CGGACACCGGTGTGCTGAGGAAACCACTACCGGATTTGAGTGAATACCTT 300  
 Db 241 CGGACACCGGTGTGCTGAGGAAACCACTACCGGATTTGAGTGAATACCTT 300  
 QY 301 TTCCAGTGTCTTCAATTCGACCTCTGCTTCATGGGACCGTGACCTCTCTGCCAGAG 360  
 Db 301 TTCCAGTGTCTTCAATTCGACCTCTGCTTCATGGGACCGTGACCTCTCTGCCAGAG 360  
 QY 361 AAACGAAACACCGGTGTGACCTGCTCATGAGGAGTTTCTTTCTAAGAGAAAAACAGTGTGC 420  
 Db 361 AAACGAAACACCGGTGTGACCTGCTCATGAGGAGTTTCTTTCTAAGAGAAAAACAGTGTGC 420  
 QY 421 TCTGTAGTAACTGTAAAGAAAGCTGAGAGTGCAGCAAGTTGGCTTACCCAGATTGAG 480  
 Db 421 TCTGTAGTAACTGTAAAGAAAGCTGAGAGTGCAGCAAGTTGGCTTACCCAGATTGAG 480  
 QY 481 AAT 483  
 Db 481 AAT 483

RESULT 2  
 AR174442  
 LOCUS AR174442 483 bp DNA linear PAT 17-DEC-2001  
 DEFINITION Sequence 1 from patent US 6306820.  
 ACCESSION AR174442  
 VERSION AR174442 1 GI:17914762  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unclassified.  
 REFERENCE 1 (bases 1 to 483)  
 AUTHORS Bend-It, A.M., Senneville, R.M. and Edwards III, C.K.  
 TITLE Combination therapy using a TNF binding protein for treating  
 TNF-mediated diseases  
 JOURNAL Parent: US 6306820-A 1 23-OCT-2001;  
 FEATURES  
 Location/Qualifiers  
 source  
 1..483  
 /organism="unknown"

BASE COUNT 130 a 124 c 123 g 106 t  
 ORIGIN  
 Query Match 100.0%; Score 483; DB 6; Length 483;  
 Best Local Similarity 100.0%; Pred. No. 5, 2e-141;  
 Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GATAGTGTGTGTCCTCCCAAGGAAAAATATATACACCTCCAAATATATGATTGCTGTACC 60  
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 Db 61 AAGTGTCCCAAAAGGAACTTATTGTACATGATGTGTCAGGCGCGGAGGATACGGAC 120  
 QY 121 TGCAGGAGGTGTGAGACCGGCTCTTACACCGCTTCAGAAAAACCACTCGACACTGCCCTC 180  
 Db 121 TGCAGGAGGTGTGAGACCGGCTCTTACACCGCTTCAGAAAAACCACTCGACACTGCCCTC 180  
 QY 181 AGCTGTCCAAATCCGAAAGAAATGGTCCAGTGAATCTCTTTGCAACAGTGGAC 240  
 Db 181 AGCTGTCCAAATCCGAAAGAAATGGTCCAGTGAATCTCTTTGCAACAGTGGAC 240  
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 Db 241 CGGACACCGGTGTGCTGAGGAAACCACTACCGGATTTGAGTGAATACCTT 300  
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 Db 301 TTCCAGTGTCTTCAATTCGACCTCTGCTTCATGGGACCGTGACCTCTCTGCCAGAG 360  
 QY 361 AAACGAAACACCGGTGTGACCTGCTCATGAGGAGTTTCTTTCTAAGAGAAAAACAGTGTGC 420  
 Db 361 AAACGAAACACCGGTGTGACCTGCTCATGAGGAGTTTCTTTCTAAGAGAAAAACAGTGTGC 420  
 QY 421 TCTGTAGTAACTGTAAAGAAAGCTGAGAGTGCAGCAAGTTGGCTTACCCAGATTGAG 480  
 Db 421 TCTGTAGTAACTGTAAAGAAAGCTGAGAGTGCAGCAAGTTGGCTTACCCAGATTGAG 480  
 QY 481 AAT 483  
 Db 481 AAT 483

RESULT 3  
 AR131310  
 LOCUS AR131310 1301 bp DNA linear PAT 16-MAY-2001  
 DEFINITION Sequence 7 from patent US 6193972.  
 ACCESSION AR131310  
 VERSION AR131310.1 GI:14120213  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unclassified.  
 REFERENCE 1 (bases 1 to 1301)  
 AUTHORS Campbell, R.K., Jameson, B.A. and Chappel, S.C.  
 TITLE Hybrid heterodimeric protein hormone  
 JOURNAL Patent: US 6193972-A 7 27-FEB-2001;  
 FEATURES  
 Location/Qualifiers  
 source  
 1..1301  
 /organism="unknown"

BASE COUNT 269 a 413 c 351 g 268 t  
 ORIGIN  
 Query Match 100.0%; Score 483; DB 6; Length 1301;  
 Best Local Similarity 100.0%; Pred. No. 5, 9e-141;  
 Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GATAGTGTGTGTCCTCCCAAGGAAAAATATATACACCTCCAAATATATGATTGCTGTACC 60  
 Db 345 GATAGTGTGTGTCCTCCCAAGGAAAAATATATACACCTCCAAATATATGATTGCTGTACC 404  
 QY 61 AAGTGTCCCAAAAGGAACTTATTGTACATGATGTGTCAGGCGCGGAGGATACGGAC 120  
 Db 405 AAGTGTCCCAAAAGGAACTTATTGTACATGATGTGTCAGGCGCGGAGGATACGGAC 464  
 QY 121 TGCAGGAGGTGTGAGACCGGCTCTTACACCGCTTCAGAAAAACCACTCGACACTGCCCTC 180  
 Db 465 TGCAGGAGGTGTGAGACCGGCTCTTACACCGCTTCAGAAAAACCACTCGACACTGCCCTC 524